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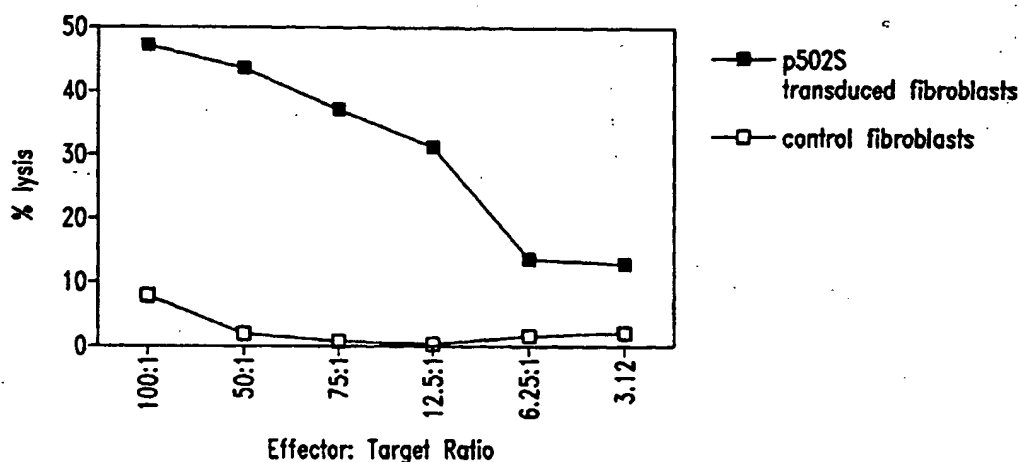
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(54) Title: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.

## COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER

### TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating

such cancers. The present invention fulfills these needs and further provides other related advantages.

#### SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a prostate tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a tumor protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and a non-specific immune response enhancer.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a non-specific immune response enhancer.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a non-specific immune response enhancer.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.



Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount

detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate tumor polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate tumor polypeptide P502S. In each case, the number of  $\gamma$ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/*neu*.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate tumor polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8<sup>+</sup> cell line (3A-1) for a representative prostate tumor antigen (P501S). Figure 6A shows the results of a <sup>51</sup>Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16

SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1

SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9

SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4

SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17

SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17

SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12

SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12

SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862

SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862

SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13

SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13

SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19

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SEQ ID NO: 50 is the determined cDNA sequence for P38

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SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36  
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38  
SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39  
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40  
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41  
SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42  
SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45  
SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46  
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51  
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56  
SEQ ID NO: 247 is the determined cDNA sequence for PTPN64  
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65  
SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67  
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76  
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84  
SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85  
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86  
SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87  
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88  
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1  
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2  
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2

SEQ ID NO: 259 is the determined cDNA sequence for JP1B1  
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2  
SEQ ID NO: 261 is the determined cDNA sequence for JP1D3  
SEQ ID NO: 262 is the determined cDNA sequence for JP1A4  
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5  
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6  
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6  
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5  
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6  
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8  
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7  
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9  
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10  
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9  
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12  
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12  
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11  
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11  
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12  
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12  
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12  
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2  
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1  
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2  
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3  
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4  
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3  
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4  
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6  
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6

SEQ ID NO: 289 is the determined cDNA sequence for JP8F5  
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8  
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7  
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7  
SEQ ID NO: 293 is the determined cDNA sequence for P8D8  
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7  
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8  
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8  
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10  
SEQ ID NO: 298 is the determined cDNA sequence for JP8C10  
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9  
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10  
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9  
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9  
SEQ ID NO: 303 is the determined cDNA sequence for JP8C12  
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11  
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12  
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12  
SEQ ID NO: 307 is the determined cDNA sequence for P711P  
SEQ ID NO: 308 is the determined cDNA sequence for P712P  
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23  
SEQ ID NO: 310 is the determined cDNA sequence for P774P  
SEQ ID NO: 311 is the determined cDNA sequence for P775P  
SEQ ID NO: 312 is the determined cDNA sequence for P715P  
SEQ ID NO: 313 is the determined cDNA sequence for P710P  
SEQ ID NO: 314 is the determined cDNA sequence for P767P  
SEQ ID NO: 315 is the determined cDNA sequence for P768P  
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes  
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5  
SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5

SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26

SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26

SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23

SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23

SEQ ID NO: 332 is the determined full length cDNA sequence for P509S

SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)

SEQ ID NO: 334 is the determined cDNA sequence for P714P

SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)

SEQ ID NO: 336 is the predicted amino acid sequence for P705P

SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10

SEQ ID NO: 338 is the amino acid sequence of the peptide p5

SEQ ID NO: 339 is the predicted amino acid sequence of P509S

SEQ ID NO: 340 is the determined cDNA sequence for P778P

SEQ ID NO: 341 is the determined cDNA sequence for P786P

SEQ ID NO: 342 is the determined cDNA sequence for P789P

SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)

SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteosome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.



SEQ ID NO: 381 is the determined cDNA sequence for B716P.  
SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.  
SEQ ID NO: 383 is the predicted amino acid sequence for P711P.  
SEQ ID NO: 384 is the cDNA sequence for P1000C.  
SEQ ID NO: 385 is the cDNA sequence for CGI-82.  
SEQ ID NO:386 is the cDNA sequence for 23320.  
SEQ ID NO:387 is the cDNA sequence for CGI-69.  
SEQ ID NO:388 is the cDNA sequence for L-iditol-2-dehydrogenase.  
SEQ ID NO:389 is the cDNA sequence for 23379.  
SEQ ID NO:390 is the cDNA sequence for 23381.  
SEQ ID NO:391 is the cDNA sequence for KIAA0122.  
SEQ ID NO:392 is the cDNA sequence for 23399.  
SEQ ID NO:393 is the cDNA sequence for a previously identified gene.  
SEQ ID NO:394 is the cDNA sequence for HCLBP.  
SEQ ID NO:395 is the cDNA sequence for transglutaminase.  
SEQ ID NO:396 is the cDNA sequence for a previously identified gene.  
SEQ ID NO:397 is the cDNA sequence for PAP.  
SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.  
SEQ ID NO:399 is the cDNA sequence for hTGR.  
SEQ ID NO:400 is the cDNA sequence for KIAA0295.  
SEQ ID NO:401 is the cDNA sequence for 22545.  
SEQ ID NO:402 is the cDNA sequence for 22547.  
SEQ ID NO:403 is the cDNA sequence for 22548.  
SEQ ID NO:404 is the cDNA sequence for 22550.  
SEQ ID NO:405 is the cDNA sequence for 22551.  
SEQ ID NO:406 is the cDNA sequence for 22552.  
SEQ ID NO:407 is the cDNA sequence for 22553.  
SEQ ID NO:408 is the cDNA sequence for 22558.  
SEQ ID NO:409 is the cDNA sequence for 22562.  
SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.  
SEQ ID NO:412 is the cDNA sequence for 22568.  
SEQ ID NO:413 is the cDNA sequence for 22570.  
SEQ ID NO:414 is the cDNA sequence for 22571.  
SEQ ID NO:415 is the cDNA sequence for 22572.  
SEQ ID NO:416 is the cDNA sequence for 22573.  
SEQ ID NO:417 is the cDNA sequence for 22573.  
SEQ ID NO:418 is the cDNA sequence for 22575.  
SEQ ID NO:419 is the cDNA sequence for 22580.  
SEQ ID NO:420 is the cDNA sequence for 22581.  
SEQ ID NO:421 is the cDNA sequence for 22582.  
SEQ ID NO:422 is the cDNA sequence for 22583.  
SEQ ID NO:423 is the cDNA sequence for 22584.  
SEQ ID NO:424 is the cDNA sequence for 22585.  
SEQ ID NO:425 is the cDNA sequence for 22586.  
SEQ ID NO:426 is the cDNA sequence for 22587.  
SEQ ID NO:427 is the cDNA sequence for 22588.  
SEQ ID NO:428 is the cDNA sequence for 22589.  
SEQ ID NO:429 is the cDNA sequence for 22590.  
SEQ ID NO:430 is the cDNA sequence for 22591.  
SEQ ID NO:431 is the cDNA sequence for 22592.  
SEQ ID NO:432 is the cDNA sequence for 22593.  
SEQ ID NO:433 is the cDNA sequence for 22594.  
SEQ ID NO:434 is the cDNA sequence for 22595.  
SEQ ID NO:435 is the cDNA sequence for 22596.  
SEQ ID NO:436 is the cDNA sequence for 22847.  
SEQ ID NO:437 is the cDNA sequence for 22848.  
SEQ ID NO:438 is the cDNA sequence for 22849.  
SEQ ID NO:439 is the cDNA sequence for 22851.  
SEQ ID NO:440 is the cDNA sequence for 22852.

SEQ ID NO:441 is the cDNA sequence for 22853.  
SEQ ID NO:442 is the cDNA sequence for 22854.  
SEQ ID NO:443 is the cDNA sequence for 22855.  
SEQ ID NO:444 is the cDNA sequence for 22856.  
SEQ ID NO:445 is the cDNA sequence for 22857.  
SEQ ID NO:446 is the cDNA sequence for 23601.  
SEQ ID NO:447 is the cDNA sequence for 23602.  
SEQ ID NO:448 is the cDNA sequence for 23605.  
SEQ ID NO:449 is the cDNA sequence for 23606.  
SEQ ID NO:450 is the cDNA sequence for 23612.  
SEQ ID NO:451 is the cDNA sequence for 23614.  
SEQ ID NO:452 is the cDNA sequence for 23618.  
SEQ ID NO:453 is the cDNA sequence for 23622.  
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.  
SEQ ID NO:455 is the cDNA sequence for LIM protein.  
SEQ ID NO:456 is the cDNA sequence for a known gene.  
SEQ ID NO:457 is the cDNA sequence for a known gene.  
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.  
SEQ ID NO:459 is the cDNA sequence for 23045.  
SEQ ID NO:460 is the cDNA sequence for 23032.  
SEQ ID NO:461 is the cDNA sequence for 23054.  
SEQ ID NOs:462-467 are cDNA sequences for known genes.  
SEQ ID NOs:468-471 are cDNA sequences for P710P.  
SEQ ID NO:472 is a cDNA sequence for P1001C.  
SEQ ID NO:473 is the amino acid sequence for PSMA.  
SEQ ID NO:474 is the amino acid sequence for PAP.  
SEQ ID NO:475 is the amino acid sequence for PSA.  
SEQ ID NO:476 is the amino acid sequence for a fusion protein containing PSA, P703P and P501S.

## DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate tumor protein or a variant thereof. A "prostate tumor protein" is a protein that is expressed in prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain prostate tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human prostate tumor proteins. Sequences of polynucleotides encoding certain tumor proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Sequences of polypeptides comprising at least a portion of a tumor protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

## PROSTATE TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate tumor protein or a portion thereof.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions,

usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are

capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Syntehi microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (e.g., a prostate tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with  $^{32}\text{P}$ ) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full-length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.



One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate tumor protein are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Isolation of these polynucleotides is described below. Each of these prostate tumor proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may

also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

#### PROSTATE TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate tumor protein or a variant thereof, as described herein. As noted above, a "prostate tumor protein" is a protein that is expressed by prostate tumor cells. Proteins that are prostate tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera

and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most

preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophatic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophatic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression

vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be

targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

In certain embodiments, the present invention provides fusion proteins comprising a polypeptide disclosed herein together with at least one of the following known prostate antigens: prostate specific antigen (PSA); prostatic acid phosphatase (PAP); and prostate specific membrane antigen (PSMA). The protein sequences for PSMA, PAP and PSA are provided in SEQ ID NO: 473-475, respectively. In certain embodiments, the fusion proteins of the present invention comprise PSA, PAP and/or PSMA in combination with one or more of the following the inventive antigens: P501S (amino acid sequence provided in SEQ ID NO: 113); P703P (amino acid sequences provided in SEQ ID NO: 327, 329, 331); P704P (cDNA sequence provided in SEQ ID NO: 67); P712P (cDNA sequence provided in SEQ ID NO: 308); P775P (cDNA sequence provided in SEQ ID NO: 311); P776P (cDNA sequence provided in SEQ ID NO: 354); P790P (cDNA sequence provided in SEQ ID NO: 352). The amino acid sequence of a fusion protein of PSA, P703P and P501S is provided in SEQ ID NO: 476. In preferred embodiments, the inventive fusion proteins comprise one of the following combinations of antigens: PSA and P703P; PSA and P501S; PAP and P703P; PAP and P501S; PSMA and P703P; PSMA and P501S; PSA, PAP and P703P; PSA, PAP and P501S; PSA, PAP, PSMA and P703P, PSA, PAP, PSMA and P501S. One of skill in the art will appreciate that the order of polypeptides within a fusion protein can be altered without substantially changing the therapeutic, prophylactic or diagnostic properties of the fusion protein.

The fusion proteins described above are more immunogenic and will be effective in a greater number of prostate cancer patients than any of the individual components alone. The use of multiple antigens in the form of a fusion protein also lessens the likelihood of immunologic escape.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide



components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-

terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

#### BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal

indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested

by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

#### T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (*see also* U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate tumor polypeptide, polynucleotide encoding a prostate tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively,



detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a prostate tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4<sup>+</sup> and/or CD8<sup>+</sup>. Prostate tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4<sup>+</sup> or CD8<sup>+</sup> T cells that proliferate in response to a prostate tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

#### PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions

or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner

et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be

formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- $\gamma$ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6, IL-10 and TNF- $\beta$ ) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt.

MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; *see* US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific

immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into

dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc $\gamma$  receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a prostate tumor protein (or portion or other variant thereof) such that the prostate tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the prostate tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be

pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

#### CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8<sup>+</sup> cytotoxic T lymphocytes and CD4<sup>+</sup> T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The



polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g., intracutaneous,*

intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100  $\mu$ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

#### METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from

the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized

on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed

and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient is incubated with a prostate tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate tumor polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate tumor polypeptide to serve as a control. For CD4<sup>+</sup> T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8<sup>+</sup> T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a prostate tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%,



preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375 and 381. Techniques for both PCR based assays and hybridization assays are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol., 51:263, 1987; Erlich ed., PCR Technology, Stockton Press, NY, 1989*).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter

performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

#### DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate tumor protein in a biological sample. Such kits generally comprise

at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

## EXAMPLES

### EXAMPLE 1

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones

having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H<sub>2</sub>O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H<sub>2</sub>O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H<sub>2</sub>O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E.*

*coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1  $\mu$ g each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the

driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193,



respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339.

## EXAMPLE 2

### DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2  $\mu$ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR,  $\beta$ -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using  $\beta$ -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the  $\beta$ -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the  $\beta$ -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-

expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive

cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

### EXAMPLE 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to

previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor

compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor



and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both microarray technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX\_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively.

The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted

amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

#### EXAMPLE 4

##### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

#### EXAMPLE 5

##### FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were

separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JTPN23 (SEQ ID NO: 231; similarity to pig

valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be

expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350-365.

## EXAMPLE 6

### PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2.1 (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100 $\mu$ g of P2S#12 and 120 $\mu$ g of an I-A<sup>b</sup> binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL),  $2 \times 10^{-5}$  M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml  $\beta$ 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7 $\mu$ g/ml dextran sulfate and 25 $\mu$ g/ml LPS for 3 days). Six days later, cells ( $5 \times 10^5$ /ml) were restimulated with  $2.5 \times 10^6$ /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and  $3 \times 10^6$ /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells

as feeders (  $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2.1 expressing) transduced with P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2.1 molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200  $\mu$ g/ml were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2.1 were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5 $\mu$ g of P1S #10 and 120 $\mu$ g

of an I-A<sup>b</sup> binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed ( $2\mu\text{g/ml}$  P1S#10 and  $10\text{mg/ml}$   $\beta 2$ -microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of  $7\mu\text{g/ml}$  dextran sulfate and  $25\mu\text{g/ml}$  LPS for 3 days). Six days later cells ( $5 \times 10^5/\text{ml}$ ) were restimulated with  $2.5 \times 10^6/\text{ml}$  peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and  $3 \times 10^6/\text{ml}$  A2 transgenic spleen feeder cells. Cells were cultured in the presence of  $20 \text{ U/ml}$  IL-2. Cells were restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of  $30\text{U/ml}$  IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

#### EXAMPLE 7

##### ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE TUMOR POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.



Human CD8<sup>+</sup> T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8<sup>+</sup> T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a  $\gamma$ -interferon ELISPOT assay (see Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on 10<sup>4</sup> fibroblasts in the presence of 3  $\mu$ g/ml human  $\beta_2$ -microglobulin and 1  $\mu$ g/ml P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml  $\gamma$ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a  $\gamma$ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of  $\gamma$ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of  $\gamma$ -interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

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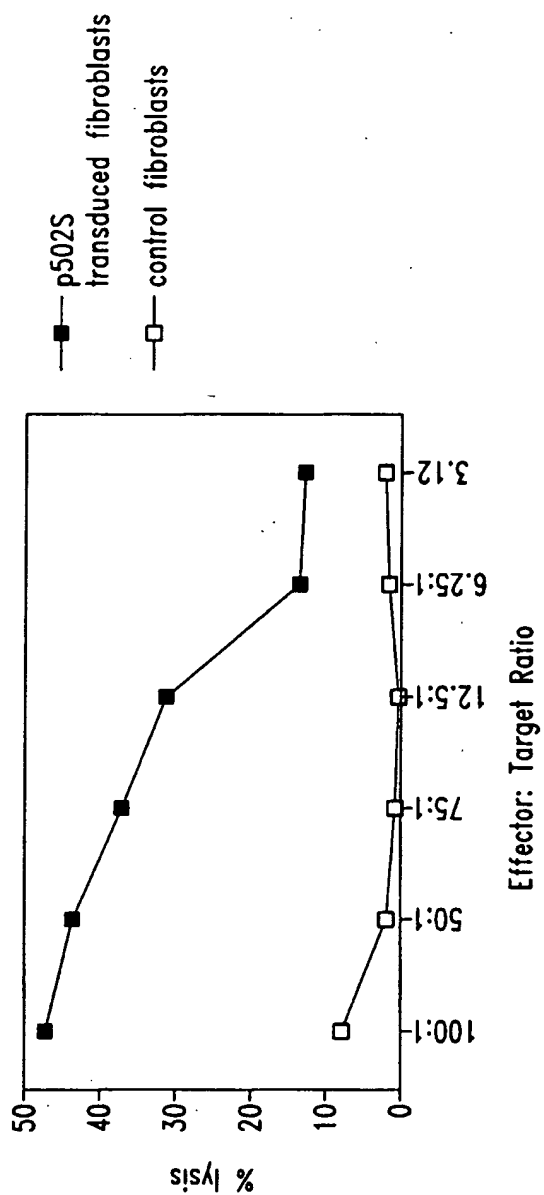
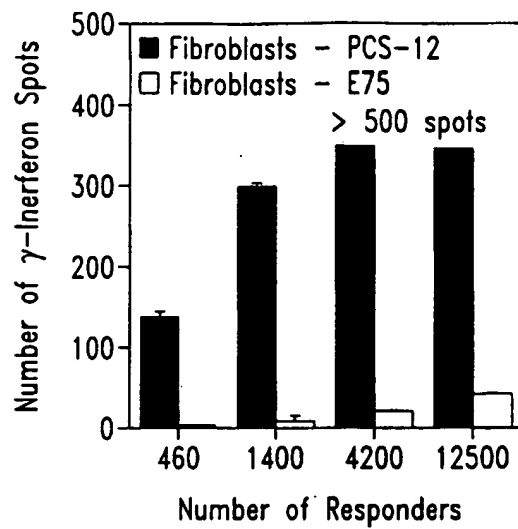
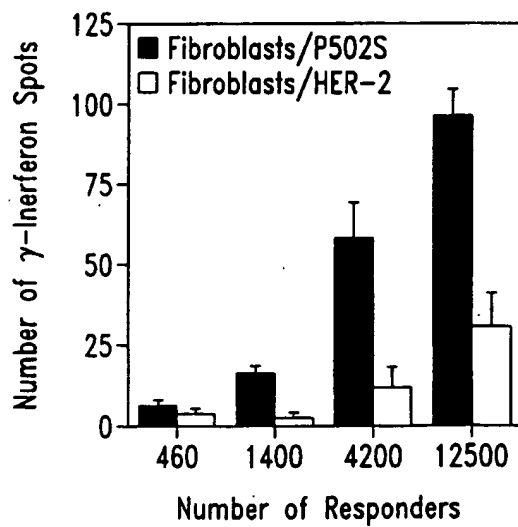


Fig. 1

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*Fig. 2A**Fig. 2B*

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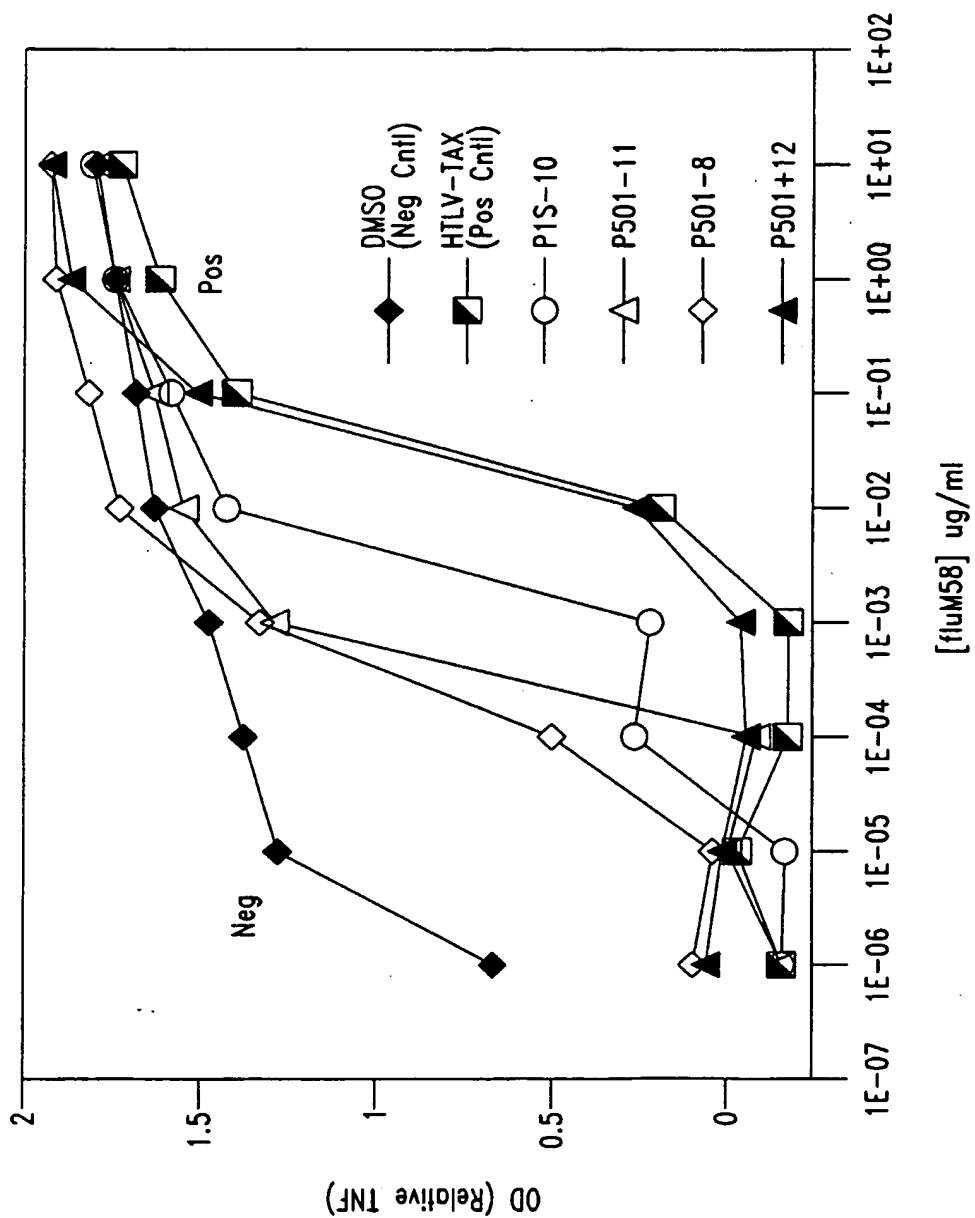


Fig. 3

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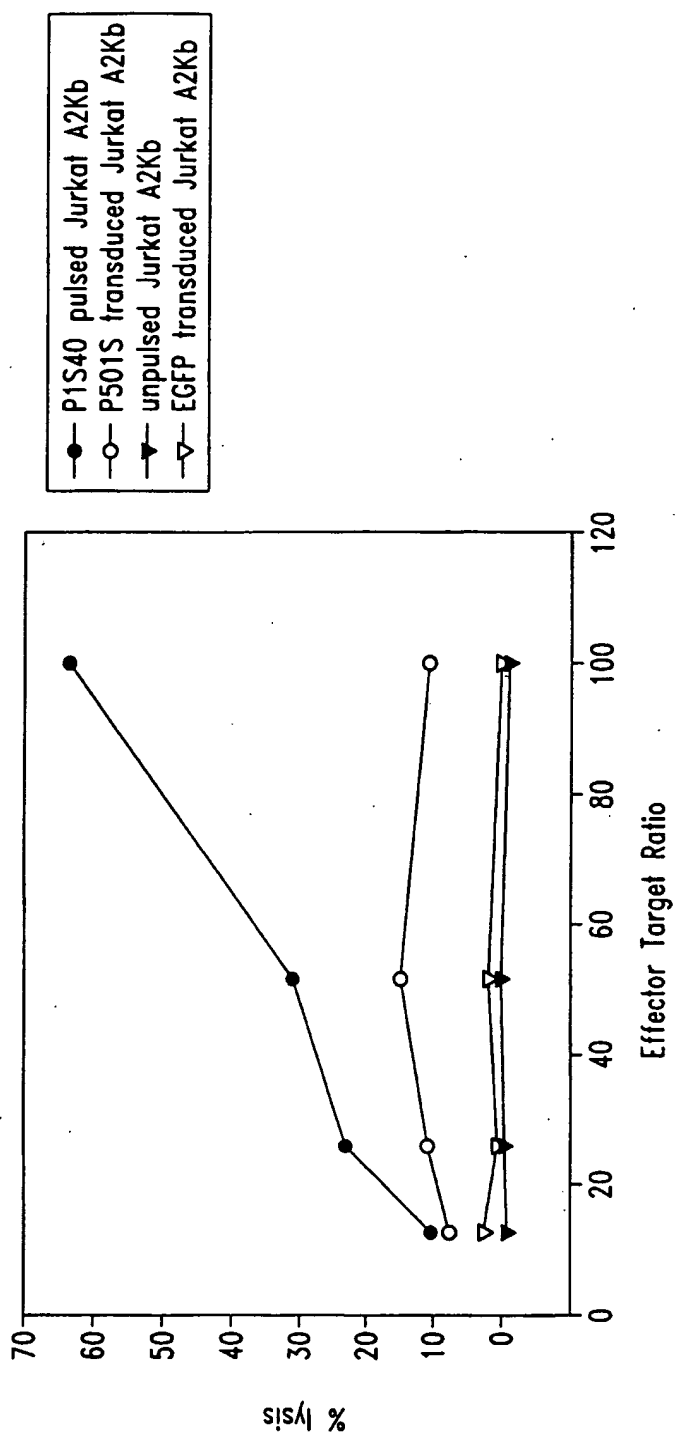


Fig. 4

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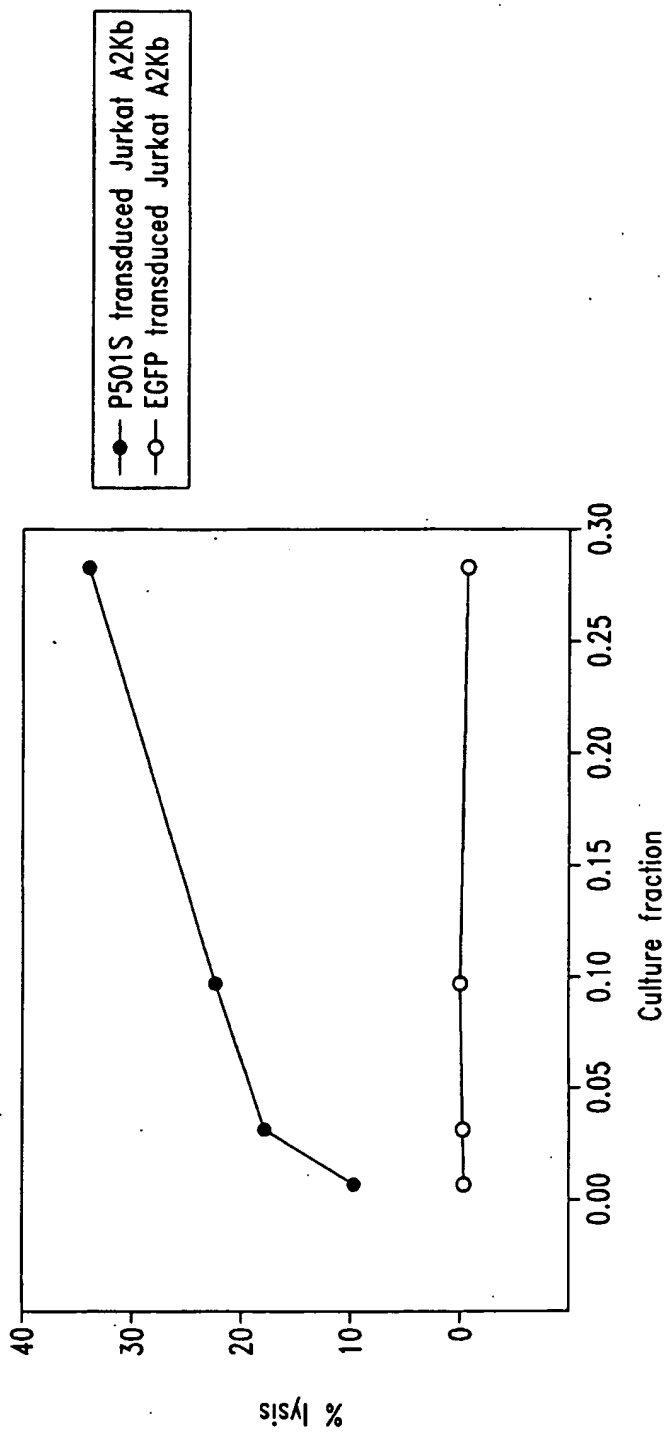
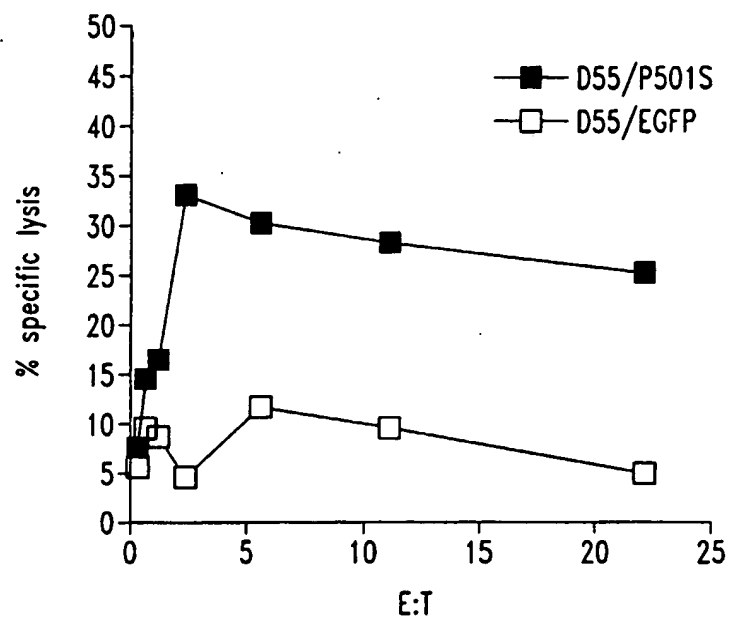
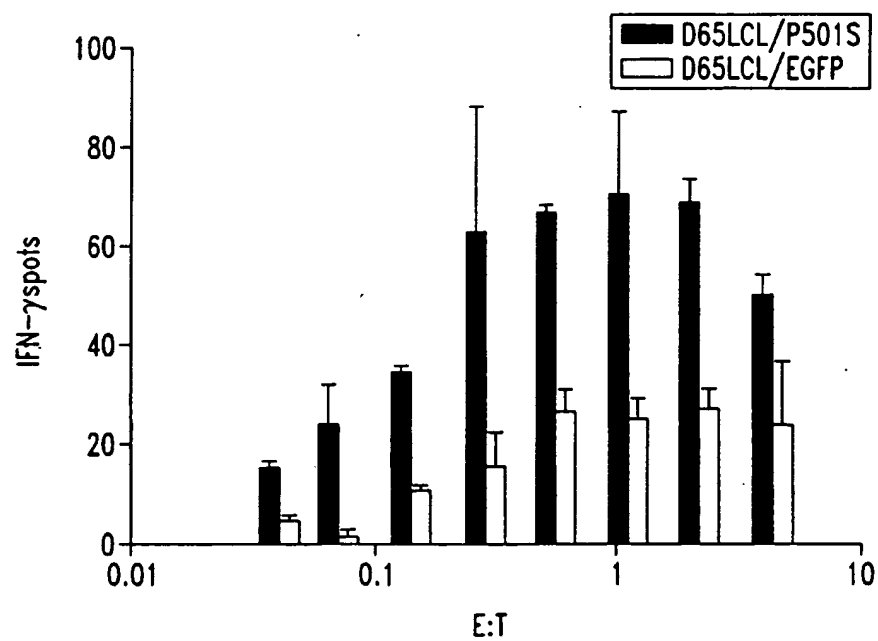


Fig. 5

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*Fig. 6A**Fig. 6B*

## SEQUENCE LISTING

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<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND  
DIAGNOSIS OF PROSTATE CANCER

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gtcattanga nggctnaaaa ggccctgtta ngggtctggg ctnggtttta cccnaccat 780  
ggaatncncc ccccggaacna ntgnatccct attcttaa 818

<210> 7  
<211> 817  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(817)  
<223> n = A,T,C or G

<400> 7  
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cgggccctat ttcaaagatt tttaggggaa ttaattctag gacgatgggt atgaaactgt 120  
ggtttgctcc acagatttca gagcattgac cgtagtatac ccccggtcgt gtagcggta 180

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aagtggtttg gtttagacgt ccggaattg catctgtttt taagcctaata gtggggacag      240
ctcatgagtg caagacgtct tgtgatgtaa ttattatacn aatgggggct tcaatcgga      300
gtactactcg attgtcaacg tcaaggagtc gcaggtcgcc tgggtctagg aataatggg      360
gaagtatgta ggaattgaag attaatccgc cgtagtcggt gttctcctag gttcaatacc      420
attggtggcc aattgatttg atggtaaggg gagggatcgt tgaactcgtc tgttatgtaa      480
aggatnccct ngggatggga aggcnatnaa ggactangga tnaatggcgg gcangatatt      540
tcaaacngtc tctanttcct gaaacgtctg aaatgttaat aanaattaan tttngttatt      600
gaatnttng gaaaaggcgt tacaggacta gaaaccaaata angaaaanta atnntaang      660
cnttatcntn aaaggnata accnctccta tnatcccacc caatngnatt cccacnenn      720
acnattggat nccccanttc canaaanggc cccccccg tgnannccnc cttttgttcc      780
cttnantgan ggttattcnc ccctngcntt atcance      817

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&lt;210&gt; 8

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(799)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 8

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catttccggg tttactttct aaggaaagcc gagcggaagc tgctaacgtg ggaatcgggtg      60
cataaggaga actttctgct ggcacgcgct agggacaagc gggagagcga ctccgagcgt      120
ctgaagcgca cgtcccagaa ggtggacttg gcaactgaaac agctgggaca catccgcgag      180
tacgaacagc gcctgaaagt gctggagcgg gaggtccagc agtgtagccg cgtcctgggg      240
tgggtggccg angcctganc cgctctgct tgcctgcccc angtgggccg ccacccctg      300
acctgcctgg gtccaaacac tgagccctgc tggcggactt caagganaac cccacangg      360
ggattttgct cctanantaa ggctcatctg ggctcggcc ccccccactg gttggccttg      420
tctttgangt gagccccatg tccatctggg ccaactgtcng gaccaccttt ngggagtgtt      480
ctccttaciaa ccacannatg cccggctcct cccggaaacc antcccanc tnggaagat      540
caagncctgn atccactnnt nctanaaccg gccnccnccg cngtggaacc cncctntgt      600
tccttttctn tnagggttaa tnncgccttg gccttncan ngctcctnnc ntttccnnt      660
gttnaaattg ttangcnccc nccnntccn cnnnnnnan cccgaccenn annttnnann      720
ncctgggggt nccnncngat tgaccenncc nccctntant tgcnttnggg nncnntgccc      780
ctttccctct nggganncg      799

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&lt;210&gt; 9

&lt;211&gt; 801

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(801)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 9

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acgccttgat cctcccaggc tgggactggt tctgggagga gccgggcatg ctgtggtttg      60
taangatgac actcccaaag gtggtcctga cagtggccca gatggacatg gggctcacct      120
caaggacaag gccaccaggt gcgggggccc aagcccacat gatccttact ctatgagcaa      180
aatccctgt gggggcttct ccttgaagtc cgccancagg gctcagtctt tggaccang      240
caggtcatgg ggttgtngnc caactggggg ccncaacgca aaanggcncg gggcctcngn      300
cacccatccc angacgcggc tacactnctg gacctccnc tccaccactt tcatgcgctg      360
ttentacccg cgnatntgtc ccantgttt cngtgccnac tccancttct nggacgtgcg      420
ctacatacgc cgggantcnc nctcccgtt tgcctctatc cagctnccan caacaaattt      480
cncntantg caccnattcc cacntttnc agntttcnc nncngcttc cttntaaaag      540
ggttganccc cgaagaaatnc cccaaaggcg gggggccngg tacccaactn cccctnata      600
gctgaantcc ccatnaccnn gnctcnatgg anccntcct ttaannaen ttctnaactt      660
gggaananc ctcgnccntn ccccnnttaa tccnccctg cnaangnnt ccccnntcc      720
nccnnntng gcntntnann cnaaaaaggc cnnnnancaa tctcctnnn cctcanttgc      780

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ccanccctcg aaatcgccn c

801

<210> 10  
 <211> 789  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(789)  
 <223> n = A,T,C or G

<400> 10  
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 acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg gttcaccttc tcagccctgc 120  
 agatccctgcc ctacacactg gcctccctct accaccggga gaagcagggtg ttcttgccca 180  
 aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttcctgc 240  
 caggccctaa gcctggagct cccttcctta atggacacgt ggggtgctgga ggcagtggcc 300  
 tgctcccacc tccacccgcg ctctgcgggg cctctgcctg tgatgtctcc gtacgtgtgg 360  
 tgggtgggtga gcccaccgan gccagggtgg ttccggggccg gggcatctgc ctggacctcg 420  
 ccatcctgga tagtgcttcc tegtgtccca ngtggcccca tccctgttta tgggtccat 480  
 tgtccagctc agccagtctg tcaactgccta tatggtgtct gccgcaggcc tgggtctggg 540  
 cccatttact ttgctacaca ggtantattt gacaagaacg anttggccaa atactcagcg 600  
 ttaaaaaatt ccagcaacat tgggggtgga aggcctgcct cactgggtcc aactccccgc 660  
 tcctgttaac cccatggggc tgccggcttg gccgccatt tctgttgctg ccaaantnat 720  
 gtggctctct gctgccacct gttgctggct gaagtgcnta cngcncanct nggggggtng 780  
 gnggttccc 789

<210> 11  
 <211> 772  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(772)  
 <223> n = A,T,C or G

<400> 11  
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 ttgttaaat aaataagtta aatatttaaa tgcctgtgtc tctgtgatgg caacagaagg 120  
 accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc 180  
 tgtgggctga ggggacctgg ttcttgtgtg ttgcccctca ggactcttcc cctacaaata 240  
 actttcatat gttcaaatcc catggaggag tgtttcatcc tagaaactcc catgcaagag 300  
 ctacattaaa cgaagctgca ggttaagggg cttanagatg ggaaaccagg tgactgagtt 360  
 tattcagcto ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc 420  
 ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc 480  
 ctccctgtat aagtccagac tgaaccccc ttggaaggnc tccagtcagg cagccctana 540  
 aactggggaa aaaagaaaag gacgccccan ccccagctg tgcantacg cacctcaaca 600  
 gcacagggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaact ngggggggca 660  
 accccggcac cccnangggg gttaacagga ancnnggnaa cntggaaccc aattnaggca 720  
 gggccnccac ccnaatntt gctgggaaat ttttctccc ctaaattntt tc 772

<210> 12  
 <211> 751  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(751)  
 <223> n = A,T,C or G

&lt;400&gt; 12

gccccaatc	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatacaaa	60
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ttggctgtgt	tgggtgacgtt	gtcattgcaa	cagaatgggg	gaaaggcact	gttctctttg	180
aagtanggtg	agtcctcaaa	atccgtatag	ttggtgaagc	cacagcactt	gagccctttc	240
atgggtgggt	tccacacttg	agtgaagtct	tcctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	ggaagtgtct	agccattgtg	gtgtacacca	aggcgaccac	360
agcagctgcn	acctcagcaa	tgaagatgan	gaggangatg	aagaagaacg	tcncgagggc	420
acacttgctc	tcagtcttan	caccatanca	gccntgaaa	accaananca	aagaccacna	480
cncgggtgc	gatgaagaaa	tnaccccneg	ttgacaaaact	tgcatggcac	tggganccac	540
agtggcccna	aaaatcttca	aaaaggatgc	cccacnatt	gaccccccaa	atgcccactg	600
ccaacagggg	ctgccccacn	cncnnaacga	tganccnatt	gnacaagatc	tncntgggtc	660
tnatnaacnt	gaaccctgcn	tngtggctcc	tgttcaggnc	cnnngcctga	cttctnaann	720
aangaactcn	gaagncccca	cngganannc	g			751

&lt;210&gt; 13

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(729)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 13

gagccaggcg	tcctctgccc	tgcccactca	gtggcaacac	ccgggagctg	ttttgtcctt	60
tgtggancct	cagcagtncc	ctctttcaga	actcantgcc	aaganccctg	aacaggagcc	120
accatgcagt	gcttcagctt	cattaagacc	atgatgatcc	tcttcaattt	gtcatctttt	180
ctgtgtggtg	cagccctggt	ggcagtgggc	atctgggtgt	caatcgatgg	ggcatccttt	240
ctgaagatct	tcggggccact	gtcgtccagt	gccatgcagt	ttgtcaacgt	gggctacttc	300
ctcatcgag	ccggcggtgt	ggtcttagct	ctaggtttcc	tgggctgcta	tgggtgctaag	360
actgagagca	agtgtgccct	cgtgacgttc	ttcttcaccc	tcctcctcat	cttcattgct	420
gaggttgcaa	tgtgtgggtc	gccttggtgt	acaccacaat	ggctgagcac	ttcctgacgt	480
tgtgtgtaat	gcctgccatc	aanaaaagat	tatgggttcc	caggaanact	tcactcaagt	540
gttggaaacac	caccatgaaa	gggctcaagt	gctgtggctt	cnnccaacta	tacggatttt	600
gaagantcac	ctacttcaaa	gaaaanagtg	cctttccccc	atttctgttg	caattgacaa	660
acgtcccca	cacagccaat	tgaaaacctg	cacccaaccc	aaanggggtc	ccaaccanaa	720
attnaagg						729

&lt;210&gt; 14

&lt;211&gt; 816

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(816)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 14

tgctcttcc	caaagtgtgt	cttgttgcca	taacaaccac	cataggtaaa	gcgggagcag	60
tgctcgctga	aggggttgta	gtaccagcgc	gggatgctct	ccttgacag	tcctgtgtct	120
ggcaggtcca	cgagtgccc	tttgtcactg	gggaaatgga	tgcgctggag	ctcgtcaaa	180
ccactcgtgt	atttttcaca	ggcagcctcg	tcgacgcgt	cggggcagtt	gggggtgtct	240
tcacactcca	ggaaactgtc	natgcagcag	ccattgctgc	agcggaactg	ggtgggctga	300
cangtgccag	agcacactgg	atggcgctt	tcctatgnan	gggcccctng	ggaaagtccc	360
tganccccc	anctgcctct	caaanccccc	accttgacac	ccccgacagg	ctagaatgga	420
atcttcttcc	cgaaaggtag	ttnttcttgt	tgcccaancc	anccccntaa	acaaactctt	480
gcanatctgc	tcgngggggg	tcntantacc	ancgtgggaa	aagaacccca	ggcngcgaac	540
caancttgtt	tggatnccgaa	gcnataatct	nctnttctgc	ttgggtggaca	gcaccantna	600

ctgtnnanct	ttagncntg	gtcctcntgg	gttggncttg	aacctaatcn	ccnntcaact	660
gggacaaggt	aantngccnt	ccttttnaatt	cccnancntn	ccccctgggt	tgggggtttt	720
cncnctccta	ccccagaaan	nccgtgttcc	cccccaacta	ggggccnaaa	ccnnttnttc	780
cacaaccctn	ccccaccac	gggttcngnt	ggttng			816

<210> 15  
 <211> 783  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(783)  
 <223> n = A,T,C or G

<400> 15						
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atgtggaaaa	cacagattgg	cgctactgc	ggggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaaggaang	cacctacctg	ttccagctga	180
cagtgactag	ctcagaccac	ccagaggaca	cggccaacgt	cacagtcaact	gtgctgtcca	240
ccaagcagac	agaagactac	tgcctcgcat	ccaacaangt	gggtcgctgc	cggggctctt	300
tcccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttcgtt	tatggaggct	360
gcttgggcaa	caagaacaac	taccttcggg	aagaagagt	cattctancc	tgtcnggggtg	420
tgcaaggtgg	gcctttgana	ngcanctctg	gggctcangc	gactttcccc	cagggccctt	480
ccatggaaa	gagccatcca	ntgttctctg	gcacctgtca	gcccaccag	ttccgctgca	540
ncaatggctg	ctgcactnac	antttcctng	aattgtgaca	acacccccca	ntgcccccaa	600
ccctcccaac	aaagcttccc	tgtnaaaaa	tacnccantt	ggcttttnac	aaacncccg	660
cncctcctt	ttccccnntn	aacaaagggc	nctngctttt	gaactgccn	aaccnnggaa	720
tctnccnngg	aaaaantncc	ccccctgggt	cctnnaance	cctccncaa	anctncccc	780
ccc						783

<210> 16  
 <211> 801  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(801)  
 <223> n = A,T,C or G

<400> 16						
gccccaatc	cagctgccac	accaccacg	gtgactgcat	tagttcggat	gtcatataaa	60
agctgattga	agcaaccctc	tactttttg	tcgtgagcct	tttgcttgg	gcagggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatggg	gaaaggcact	gttctctttg	180
aagtaggggtg	agtcctcaaa	atccgtatag	ttgggtgaagc	cacagcactt	gagccctttc	240
atgggtgggtg	tccacacttg	agtgaagtct	tcctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	gaagtgtcga	gccattgtgg	tgtacaccaa	ggcgaccaca	360
gcagctgcaa	cctcagcaat	gaagatgagg	aggaggatga	agaagaacgt	cncgagggca	420
cacttgctct	ccgtcttagc	accatagcag	cccangaaac	caagagcaaa	gaccacaacg	480
ccngctgcca	atgaaagaaa	ntaccacgt	tgacaaactg	catggccact	ggacgacagt	540
tgggccgaan	atcttcagaa	aagggatgcc	ccatcgattg	aacaccana	tgcccactgc	600
cnacaggggtg	gcncncncn	gaaagaatga	gccattgaag	aaggatcnc	ntggtcttaa	660
tgaactgaaa	ccntgcatgg	tgggccctgt	tcagggctct	tggcagtga	ttctganaaa	720
aaggaaacngc	ntnagcccc	ccaaangana	aaacaccccc	gggtgttgcc	ctgaattggc	780
ggccaaggan	ccctgccccn	g				801

<210> 17  
 <211> 740  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(740)  
 <223> n = A,T,C or G

<400> 17  
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 cctttgtgga gcctcagcag ttccctcttt cagaactcac tgccaagagc cctgaacagg 120  
 agccaccatg cagtgcctca gcttcattaa gaccatgatg atcctcttca atttgctcat 180  
 ctttctgtgt ggtgcagccc tgttggcagt gggcatctgg gtgtcaatcg atggggcatc 240  
 ctttctgaag atcttcgggc cactgtcgtc cagtgccatg cagtttgta acgtgggcta 300  
 cttcctcatc gcagccggcg ttgtggtcct tgctcttggg ttccctgggct gctatgggtg 360  
 taagacggag agcaagtgtg ccctcgtgac gttcttcttc atcctcctcc tcatcttcat 420  
 tgctgaagtt gcagctgctg tggctgcctt ggtgtacacc acaatggctg aaccattcct 480  
 gacgttgctg gtantgcctg ccatcaanaa agattatggg ttcccaggaa aaattcactc 540  
 aantntggaa caccnccatg aaaagggctc caatttctgn tggcttcccc aactataccg 600  
 gaattttgaa agantcncctc tacttccaaa aaaaaanant tgcttttnc cccnttctgt 660  
 tgcaatgaaa acntcccaan acngccaatn aaaacctgcc cnnncaaaaa ggntcncaaa 720  
 caaaaaaant nnaagggttn 740

<210> 18  
 <211> 802  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(802)  
 <223> n = A,T,C or G

<400> 18  
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 caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcatatg 120  
 ggatacactt tacttttagca gccagggtga caactgagag gtgtcgaagc ttattcttct 180  
 gagcctctgt tagtgaggga agattccggg cttcagctaa gtagtcagcg tatgtcccat 240  
 aagcaaacac tgtgagcagc cggaaggtag aggcaaatgc actctcagcc agctctctaa 300  
 cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat 360  
 ggatgagtgt ggccagcgtt gcccccttgg ccgacttggc taggagcaga aattgctcct 420  
 ggttctgccc tgtcaccttc acttccgcac tcatcactgc actgagtgtg ggggacttgg 480  
 gctcaggatg tccagagacg tggttccgcc ccctcnctta atgacaccgn ccanncaacc 540  
 gtcgggtccc gccgantgng ttctgctgnc ctgggtcagg gtctgctggc cnetacttgc 600  
 aancttctgc nggcccattg aattcaccnc accggaactn gtangatcca ctntttctat 660  
 aaccggnccg caccgcnntt ggaactccac tcttntncc ttacttgag ggtaaggtc 720  
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 tnccancnc atangaagcc ng 802

<210> 19  
 <211> 731  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(731)  
 <223> n = A,T,C or G

<400> 19  
 cnaagcttcc aggtnacggg ccgcnancc tgaccnagg tancanaang cagnncgagg 60  
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 cntgacccca actcccncc ncnantgca gtgatgagt cagaactgaa ggtnacgtgg 180  
 caggaaccaa gancaaannc tgctcnnct caagtcggcn nagggggcgg ggctggccac 240  
 gncatcent cnagtgtgtn aaagcccn cctgtctact tgtttggaga acngcnnga 300

catgccagn	gttanataac	nggcngagag	tnantttgcc	tctcccttcc	ggctgcgean	360
cgngtntgct	tagnggacat	aacctgacta	cttaactgaa	cccnngaate	tnccnccct	420
ccactaagct	cagaacaaaa	aacttcgaca	ccactcantt	gtcacctgnc	tgctcaagta	480
aagtgtaccc	catncccaat	gtntgctnga	ngctctgncc	tgcnttangt	tcggtcctgg	540
gaagacctat	caattnaagc	tatgtttctg	actgcctctt	gctccctgna	acaancnacc	600
cnncnntcca	agggggggnc	ggcccccaat	ccccccaacc	ntnaattnan	tttancccn	660
ccccnggcc	cggcctttta	cnancntcnn	nnacngggna	aaaccnngc	tttncccaac	720
nnaatccncc	t					731

<210> 20  
 <211> 754  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc feature  
 <222> (1)...(754)  
 <223> n = A,T,C or G

<400> 20						
tttttttttt	tttttttttt	taaaaacccc	ctccattnaa	tgnaaaacttc	cgaaattgtc	60
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annttaaatt	aaatnttntt	tgngngnnna	ancnnaatgt	nangaaagtt	naaccanta	180
tnancttnaa	tncttgga	ccngtngntt	ccaaaaatnt	ttaaccctta	antccctccg	240
aaatngttna	nggaaaacc	aantttctnt	aaggttgttt	gaaggntnaa	tnaaaanccc	300
nnccaattgt	ttttngccac	gcctgaatta	attggnttcc	gntgttttcc	nttaaaanaa	360
ggnnancccc	ggttantnaa	tccccccnnc	cccaattata	ccganttttt	ttngaattgg	420
gancccnccg	gaattaacgg	ggnnnttccc	tnttgggggg	cnngnncccc	cccntcggg	480
ggttngggnc	aggnncnaat	tgtttaaggg	tccgaaaaat	ccctccnaga	aaaaaanctc	540
ccaggntgag	nnnnggggtt	cccccccccc	cangggccct	ctcgnaagtt	tggggtttgg	600
ggggcctggg	atttnttttc	ccctntttnc	tcccccccc	ccngggganag	aggttngngt	660
tttgntcnnc	ggccccnccn	aaganctttn	ccganttnan	ttaaatccnt	gcctnggcga	720
agtcctttgn	agggntaaan	ggccccctnn	cggg			754

<210> 21  
 <211> 755  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc feature  
 <222> (1)...(755)  
 <223> n = A,T,C or G

<400> 21						
atcancccaat	gaccccaaac	nnngggaccnc	tcanccggncc	nnncnaccnc	cggccnatca	60
nnngtnagnnc	actncnnttn	natcacnccc	cnccnactac	gcccnncnanc	cnacgcncta	120
nncanatncc	actganngcg	cgangtngan	ngagaaanct	nataccanag	ncaccanacn	180
ccagctgtcc	nanaangcct	nnnatacnng	nnnatccaat	ntgnancctc	cnaagtattn	240
nncnncanac	gattttcctn	anccgattac	ccntncccc	tanccctcc	cccccaacna	300
cgaaggcnct	ggncnaagg	nngecncc	ccgtagntc	cccncaagt	cncncccta	360
aactcancn	nattacncc	ttcntgagta	tcactcccc	aatctcaccc	tactcaactc	420
aaaaanaten	gatacaaat	aatncaagc	tgnttatnac	actntgactg	ggtctctatt	480
ttagnggtcc	ntnaancntc	ctaatacttc	cagtctncct	tcnccaattt	ccnaanggct	540
ctttcngaca	gcantttttg	gttcccnntt	gggttcttan	ngaattgccc	ttcntngaac	600
gggtctntct	tttccttcgg	ttancctggn	ttcnccggc	cagttattat	ttccntttt	660
aaattcntnc	cntttanttt	tggcnttca	aacccccggc	cttgaaaacg	gccccctggt	720
aaaaggttgt	tttganaaaa	ttttgtttt	gttcc			755

<210> 22  
 <211> 849  
 <212> DNA



<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(849)

<223> n = A,T,C or G

<400> 22

tttttttttt	tttttangtg	tngtcgtgca	ggtagaggct	tactacaant	gtgaanacgt	60
acgctnggan	taangcgacc	cgantttctag	gannncacct	aaaatcanac	tgtgaagatn	120
atcctgnnna	cggaanggtc	accggnngat	nntgctaggg	tgncnctcc	cannncnttn	180
cataactcng	nggccctgcc	caccaccttc	ggcgccccng	ngnccgggcc	cggttcattn	240
gnnttaaccn	cactnngcna	ncggtttccn	nccccnncng	accnngggga	tccgggggtnc	300
tctgtcttcc	cctgnagncn	anaaantggg	ccnccggnccc	ctttaccctt	nnacaagcca	360
cngccttcta	ncnncngccc	cccctccant	nnngggggact	gccnanngct	ccgttncntng	420
nnaccccnnn	gggtncctcg	gttgtcgant	cnaccgnang	ccanggattc	cnaaggaagg	480
tgcgttnttg	ggccctaccc	ttcgctncgg	nnacaccttc	ccgacnanga	nccgtcccg	540
cnncnccngg	cctcncctcg	caacacccgc	netentcngt	ncggnnnccc	ccccacccgc	600
nccctcncnc	ngnccgnanc	ctccnccncc	gtctcannca	ccaccccgcc	ccgccaggcc	660
ntcanccacn	ggnggacnng	nagcncnttc	gcncgcgcgn	gcgnccacct	cgccncngaa	720
ctnctcngg	ccantnncgc	tcaancnna	cnaaacgcgc	ctgcgcggcc	cgnagcgncc	780
ncctccncga	gtcctcccg	cttcnacc	angnnttcn	cgaggacacn	nnaccccgcc	840
nncangcgg						849

<210> 23

<211> 872

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(872)

<223> n = A,T,C or G

<400> 23

gcgcaaacta	tacttcgctc	gnactcgtgc	gcctcgtcnc	tcttttcttc	cgcaaccatg	60
tctgacnanc	ccgattnggc	ngatatacn	aagntcganc	agtccaaact	gantaacaca	120
cacacnncn	aganaaatcc	netgccttcc	anagtanacn	attgaacnng	agaaccangc	180
nggcgaatcg	taatnaggcg	tgcgcgcgca	atntgtcncc	gtttattntn	ccagcntcnc	240
ctnccnacc	tacntcttcn	nagctgtcnn	accctngtn	cgnaccccc	naggctggga	300
tgcgggtttn	nntgaccgng	cnccccctcc	ccccctccat	nacganccnc	ccgcaccacc	360
nanngcncgc	nccccgnct	cttcgccncc	ctgtcctntn	ccccgtngc	ctggcncngn	420
accgcattga	ccctcgccnn	ctncnngaaa	ncgnanacgt	ccgggttggn	annancgctg	480
tgggnnngcg	tctgcncgcg	gttccttcn	ncnnetcca	ccatcttcnt	tacngggctc	540
ccnccgcntc	tcnnncaacn	cctgggacgc	tntcctntgc	cccccttnac	tccccccctt	600
cgncgtgncc	cgncccccacc	ntcatttnca	nacgntcttc	acaannncct	ggntnnctcc	660
cnancngncn	gtcanccnag	ggaaggngg	ggnnccnntg	nttgacgttg	nggngangtc	720
cgaanantcc	tcnccntcan	cnetaccct	cgggcggnct	ctcngttnc	aacttancaa	780
ntctcccccg	ngngcncntc	tcagcctcnc	cnccccnct	ctctgcantg	tnetctgctc	840
tnaccnntac	gantnttcgn	cncctcttt	cc			872

<210> 24

<211> 815

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(815)

<223> n = A,T,C or G

<400> 24

gcatgcaagc	ttgagtat	tatagngtca	cctaaatanc	ttggcntaat	catggctnta	60
nctgncttcc	tgtgtcaaat	gtatacnaa	tanatatgaa	tctnatntga	caagannngta	120
tcntncatta	gtaacaantg	tnntgtccat	cctgtcngan	canattccca	tnnattnnng	180
cgcattcnnc	gncantatn	taatngggaa	ntcnntnnn	ncaccnncat	ctatcntncc	240
gncacctgac	tggnagagat	ggatnanttc	tnntntgacc	nacatgttca	tcttggattn	300
aanancccc	cgcnngccac	cggttngnng	cnagccnntc	ccaagacctc	ctgtggaggt	360
aacctgctgc	aganncatca	aacntgggaa	accgcgnncc	angtnnaagt	ngnnncanan	420
gatcccgctc	aggnttnacc	atcccttcnc	agcgccccct	ttngtgcctt	anagnnagc	480
gtgtccnanc	cnctcaacat	ganacgcgcc	agnccanccg	caattnggca	caatgtcgnc	540
gaaccccccta	gggggantna	tncaaanccc	caggattgtc	cncncangaa	atcccnanc	600
cccnccttac	ccncttttgg	gacngtgacc	aantcccggg	gtncaggtcc	ggccngnctc	660
ccccaccggt	nnccntgggg	gggtgaanct	cngnntcanc	cngncgaggn	ntcgnaagga	720
accggnccctn	ggncgaannng	ancnntcnga	agnccnntc	cgtataaccc	cccctcncca	780
nccnacngnt	agntcccccc	cngggtncgg	aangg			815

&lt;210&gt; 25

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(775)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 25

ccgagatgtc	tcgtctcgtg	gccttagctg	tgctcgcgct	actctctctt	tctggcctgg	60
aggctatcca	gcgtactcca	aagattcagg	tttactcacg	tcattccagca	gagaatggaa	120
agtcaaattt	cctgaattgc	tatgtgtctg	ggtttcatcc	atccgacatt	gaanttgact	180
tactgaagaa	tggnagaga	attgaaaaag	tgagagcattc	agacttgtct	ttcagcaagg	240
actggtcttt	ctatctcntg	tactacactg	aattcaccctc	cactgaaaaa	gatgagtatg	300
cctgccgtgt	gaaccatgtg	actttgtcac	agcccaagat	agttaagtgg	gatcgagaca	360
tgtaagcagn	cnncatggaa	gtttgaagat	gccgcatttg	gattggatga	attccaaatt	420
ctgcttgctt	gcntttta	antgatatgc	ntatacaccc	taccctttat	gncccaaat	480
tgtaggggtt	acatnantgt	tcnctnngga	catgatcttc	ctttataant	ccnccnttcg	540
aattgcccgt	cncccnngtn	ngaattgttc	cnnaaccacg	gttggctccc	ccaggtcncc	600
tcttacggaa	gggcctgggc	cnctttncaa	ggttggggga	accnaaaatt	tcnctntngc	660
cncccncca	cnntcttngn	nnccnctttt	ggaacccttc	cnattccctt	tgccctenna	720
nccttnncta	anaaaacttn	aaancgtngc	naaanntttt	acttcccccc	ttacc	775

&lt;210&gt; 26

&lt;211&gt; 820

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(820)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 26

anattantac	agtgtaatct	tttcccagag	gtgtgtanag	ggaacggggc	ctagaggcat	60
cccanagata	ncttatanca	acagtgtctt	gaccaagagc	tgctgggcac	atttcctgca	120
gaaaagggtg	cgttccccat	cactctctct	ctccccatagc	catcccagag	gggtgagtag	180
ccatcangcc	ttcgggtgga	gggagtcang	gaaacaacan	accacagagc	anacagacca	240
ntgatgacca	tgggcggggg	cgagcctctt	ccctgnaccg	gggtggcana	nganagccta	300
nctgaggggt	cacactataa	acgttaacga	ccnagatnan	cacctgcttc	aagtgcaccc	360
ttctactctg	acnaccangn	accnnnaact	gcngcctggg	gacagcnctg	ggancagcta	420
acnagacact	cactgcctcc	cccatggccg	tnccgntccc	tggtcctgnc	aagggaagct	480
ccctgttggg	attncgggga	naccaagggg	nccccctctc	ccanctgtga	aggaaaaann	540
gatggaattt	tncccttccg	gccnntcccc	tcttcttcta	cacgccccct	nttactctnc	600
tccctctntt	ntcctgncnc	acttttnacc	ccnnnatctc	ccttnattga	tcggannctn	660

ganattccac tnnccctnc cntcnatcng naanacnaaa nactntctna cccnggggat 720  
 gggnnccctcg ntcatectct ctttttctct accnccnntt ctttgcctct ccttngatca  
 780tccaaccntc gntggccntn cccccccnnn tcttttcccc  
 820

<210> 27  
 <211> 818  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc feature  
 <222> (1)...(818)  
 <223> n = A,T,C or G

<400> 27  
 tctgggtgat ggcctcttcc tctcagggga cctctgactg ctctgggcca aagaatctct 60  
 tgtttcttct ccgagcccca ggcagcgggtg attcagccct gcccaacctg attctgatga 120  
 ctgctgatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggagggggcg 180  
 ctgctgagca cttccgcccc tcaccctgcc cagccctgc catgagctct gggctgggtc 240  
 tccgctcca ggggtctgct cttccangca ngccancaa tgggcgtggg ccacactggc 300  
 ttcttctgc cccntccctg gctctganc tctgtcttcc tgtctgtgc angcncctg 360  
 gatctcagtt tccctcncctc anngaactct gtttctgann tcttcantta actntgant 420  
 tatnaccnan tggctgtnc tgtcnnactt taatgggcn gaccggctaa tccctccctc 480  
 nctcccttcc anttccnnna accngcttnc cntcntctcc ccntancccg ccnggggaanc 540  
 ctcttttgcc ctnaccangg gccnnnaccg cccntnctn ggggggcnng gtnnctnnc 600  
 ctgntnnccc cncctcncnt tncctcgtcc cnnccnccgn nngcannttc ncngtcccn 660  
 tnnctcttcc ngntcgnaa ngntcncntn tnnnnngncc ngntnntncc tccctctcnc 720  
 cnnntgnang tnnntnnncc ncngnncccc nnnccnnnnn nggnntnnn tctnccngc 780  
 cccnncccc ngnattaagg cctccnntct ccggccnc 818

<210> 28  
 <211> 731  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc feature  
 <222> (1)...(731)  
 <223> n = A,T,C or G

<400> 28  
 aggaagggcg gagggatatt gtangggatt gagggatagg agnataangg gggaggtgtg 60  
 tccaacatg anggtgngt tctcttttga angaggggtg ngtttttann ccnggtgggt 120  
 gattnaacct cattgtatgg agnnaaagg ttnagggat ttttcggctc ttatcagtat 180  
 ntanattcct gtnaatcgga aaatnatntt tcnnccggaa aatnttgctc ccatccgnaa 240  
 attnctcccg ggtagtgcatt nttngggggg cngccangtt tcccaggctg ctanaatcgt 300  
 actaaagntt naagtgggan tncaaatgaa aacctnncc agagnatccn taccgactg 360  
 tnnnttncct tcgcccctng actctgcnn agcccaatac ccnngngnat gtcncccn 420  
 nnnccgncnc tgaaannnnc tcgnggctnn gancatcang gggtttcgca tcaaaagcnn 480  
 cgtttcccat naaggcaact tngcctcctc caaccnctng ccctcnncca ttngccgctc 540  
 nggttccct acgctnnntg cncctnnntn ganattttnc ccgctnggg naancctcct 600  
 gnaatggga gggccttntc ttttnaccnn gnggtntact aatcnnctnc acgctnctt 660  
 tctcnacccc ccccttttt caatccccc ggnaatggg gtctccccnn cgangggggg 720  
 nnnccannc c 731

<210> 29  
 <211> 822  
 <212> DNA  
 <213> Homo sapien

<220>

<221> misc\_feature  
 <222> (1)...(822)  
 <223> n = A,T,C or G

<400> 29  
 actagtccag tgtggtggaa ttccattgtg ttggggncnc ttctatgant antnttagat 60  
 cgctcanacc tcacancctc ccnacnangc ctataangaa nannaataga nctgtncnnt 120  
 atntntacnc tcatannect cnnnaccacac tccctcttaa cccntactgt gcctatngcn 180  
 tnntantct ntgccgectn cnanccaccn gtggggcnac cncnngnatt ctcnatctcc 240  
 tcnccatntn gcctananta ngtncatacc ctatacctac nccaatgcta nnnctaancn 300  
 tccatnantt annntaacta ccactgacnt ngactttcnc atnanctcct aatttgaatc 360  
 tactctgact cccacngcct annnattagc anctcccccc nacnatntct caaccaaate 420  
 ntcaacaacc tatctanctg ttcnccaacc nttncctcgg atccccnnac aacccccctc 480  
 ccaaataccc nccacctgac ncctaaccn caccatcccg gcaagccnan ggncatttan 540  
 ccactggaat cacnatngga naaaaaaac ccnaactctc tancncnnat ctcccataana 600  
 aatnctcctn naatttactn ncantnccat caanccccacn tgaaacnnaa cccctgtttt 660  
 tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc ccccnctnc 720  
 ccnaatgaag gncncccaat cnangaaacg nccntgaaaa ancnaggcna anannntccg 780  
 canatcctat cccttanttn ggggnccctt nccnngggcc cc 822

<210> 30  
 <211> 787  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(787)  
 <223> n = A,T,C or G

<400> 30  
 cggccgcctg ctctggcaca tgcctcctga atggcatcaa aagtgatgga ctgcccattg 60  
 ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctcccctt 120  
 gtctgcagga tttgatgtct gaagtcgtgg agtggtggctt ggagctcctc atctacatna 180  
 gctggaagcc ctggaggggc tctctcgcca gcctccccct tctctccacg ctctccangg 240  
 acaccagggg ctccaggcag cccattattc ccagnangac atgggtgtttc tccacgcgga 300  
 cccatggggc ctgnaaggcc aggggtctcct ttgacaccat ctctcccgtc ctgcctggca 360  
 ggccgtggga tccactantt ctanaacggn cgccaccncg gtgggagctc cagcttttgt 420  
 tcccnttaat gaaggttaat tgcncgcttg gcgtaatcat nggtcanaac tnttctctgt 480  
 gtgaaattgt ttntccccct ncnattccnc ncnacatacn aacccggaan cataaagtgt 540  
 taaagcctgg gggtngcctn nngaataaac tnaactcaat taattgcgtt ggctcatggc 600  
 ccgctttccn ttcnngaaaa ctgtcntccc ctgcnttntt gaatcgggca ccccccnggg 660  
 aaaagcgggt tgcnttttng ggggntcctt ccncttcccc cctcnctaan ccctncgect 720  
 cggtcgttnc nggtngcggg gaangggnat nnnctcccnc naagggggng agnnngntat 780  
 ccccaaa 787

<210> 31  
 <211> 799  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(799)  
 <223> n = A,T,C or G

<400> 31  
 tttttttttt tttttttggc gatgctactg ttttaattgca ggaggtgggg gtgtgtgtac 60  
 catgtaccag ggctattaga agcaagaagg aaggaggagg ggcagagcgc cctgctgagc 120  
 aacaaaaggc tctctgagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct 180  
 cccgcagggt gggggccacc agtccagggg tgggagcact acanggggtg ggagtgggtg 240  
 gtggctggtg cnaatggcct gncacanatc cctacgattc ttgacacctg gatttcacca 300

ggggaccttc	tggttctccca	nggnaacttc	ntnnatctcn	aaagaacaca	actgtttctt	360
cngcanttct	ggctgttcat	ggaaagcaca	ggtgtccnat	ttnggctggg	acttgggtaca	420
tatgggtccg	gcccacctct	cccntcnaaa	aagtaattca	ccccccccc	ccntctnttg	480
cctgggccc	taantaccca	caccggaact	canttantta	ttcatcttng	gntgggcttg	540
ntnatcnccn	cctgaangcg	ccaagttgaa	aggccacgcc	gtncnccnctc	cccatagnan	600
ntttttnncn	canctaagtc	ccccccnggc	aacnatccaa	tcccccccn	tgggggcccc	660
agcccanggc	ccccgncctg	ggnnnccngn	cncgnantcc	ccaggntctc	ccantcngnc	720
ccnnngcncc	cccgcacgca	gaacanaagg	ntngagccnc	cgcannnnnn	nggtnncnac	780
ctcgccccc	ccnnccngng					799

<210> 32  
 <211> 789  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(789)  
 <223> n = A,T,C or G

<400> 32	
tttttttttt	60
tttttccnag	120
ggcaacaggc	180
cgctcccget	240
ggtgggcacc	300
nattaggaat	360
gcggtcccg	420
nccngccaca	480
ggncatgtc	540
ccaaaagtcc	600
ccccttgccc	660
tggnnggcaa	720
ntcctnnnca	780
ccccccnccg	789

<210> 33  
 <211> 793  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(793)  
 <223> n = A,T,C or G

<400> 33	
gacagaacat	60
aattcatggc	120
gactaaagtc	180
agaagtttgc	240
gcacagatgc	300
acaangaacg	360
ctctgtgtgt	420
ggncgcacc	480
tggcgtaatc	540
acaacatacg	600
nactcacatt	660
gccagctgcc	720
cgccttccc	780
acggtatcna	793

<210> 34  
 <211> 756  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(756)  
 <223> n = A,T,C or G

<400> 34  
 gccgcgaccg gcatgtacga gcaactcaag ggcgagtggg accgtaaaag ccccaatctt 60  
 ancaagtgcg gggaanagct gggtcgactc aagctagttc ttctggagct caacttcttg 120  
 ccaaccacag ggaccaagct gaccaaacag cagctaattc tggcccgtga catactggag 180  
 atcggggccc aatggagcat cctacgcaan gacatccctt ccttcgagcg ctacatggcc 240  
 cagctcaaat gctactactt tgattacaan gagcagctcc ccgagtcagc ctatatgcac 300  
 cagctcttgg gcctcaacct cctcttcctg ctgtcccaga accgggtggc tgantnccac 360  
 acgganttgg ancggctgcc tgcccaanga catacanacc aatgtctaca tcnaccacca 420  
 gtgtcctgga gcaatactga tgganggcag ctaccncaaa gtnttcctgg ccnagggtaa 480  
 catccccgcg cgagagctac accttcttca ttgacatcct gctcgacact atcagggatg 540  
 aaaatcgcn ggttgctcca gaaaggctnc aanaanatcc ttttcnctga aggccccggg 600  
 atnncctagt nctagaatcg gcccgccatc gcggtgganc ctccaacctt tcgttnccct 660  
 ttactgaggg ttnattgccg cccttggcgt tatcatggtc acnccngttn cctgtgttga 720  
 aattnttaac cccccacaat tccacgcena cattng 756

<210> 35  
 <211> 834  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(834)  
 <223> n = A,T,C or G

<400> 35  
 ggggatctct anactnacct gnatgcatgg ttgtcgggtg ggtcgctgtc gatgaanatg 60  
 aacaggatct tgcccttgaa gctctcggct gctgtnttta agttgctcag tctgccgtca 120  
 tagtcagaca cncctcttgg caaaaaacan caggatntga gtcttgattt cacctccaat 180  
 aatcttcnng gctgtctgct cggtgaactc gatgacnang ggcagctggg tgtgtntgat 240  
 aaantccanc angttctcct tggtagctc cccttcaaag ttgttccggc cttcatcaaa 300  
 cttctnnaan angannancc canctttgtc gagctggnat ttgganaaca cgtcactgtt 360  
 ggaaactgat cccaaatggt atgtcatcca tcgcctctgc tgccctgcaa aaacttgctt 420  
 ggcncaaatc cgactcccn tccttgaaag aagcconatca cccccctc cctggactcc 480  
 nncaangact ctncgcctnc cccntccnng cagggttggg ggcannccgg gccntgcgc 540  
 ttcttcagcc agttcacnat nttcatcagc ccctctgcca gctgtntat tccttggggg 600  
 ggaanccgtc tctcccttcc tgaannaact ttgaccgtng gaatagccgc gcntcnccnt 660  
 acntnctggg ccgggttcaa antccctccn ttgncnntcn cctcgggcca ttctggattt 720  
 nccnaacttt ttcttcccc cncccnccg ngtttggntt ttctatnggg ccccaactct 780  
 gctnttggcc antccctgg ggcntntan cnccectnt ggtcccntng ggcc 834

<210> 36  
 <211> 814  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(814)  
 <223> n = A,T,C or G

<400> 36

cggnccgcttt	ccngccgcgc	cccgtttcca	tgacnaagge	tcccttcang	ttaaatacn	60
cctagnaaac	attaatgggt	tgctctacta	atacatcata	cnaaccagta	agcctgcccc	120
naacgccaac	tcaggccatt	cctaccaaa	gaagaaaggc	tggtctctcc	acccctgta	180
ggaaaggcct	gccttgtaag	acaccacaat	ncggctgaat	ctnaagtctt	gtgttttact	240
aatggaaaaa	aaaaataaac	aanaggtttt	gttctcatgg	ctgcccaccg	cagcctggca	300
ctaaaacanc	ccagcgctca	cttctgcttg	ganaaatatt	ctttgctctt	ttggacatca	360
ggcttgatgg	tatcaactgcc	acntttccac	ccagctgggc	ncccttcccc	catntttgtc	420
antganctgg	aaggcctgaa	ncttagtctc	caaaagtctc	ngcccacaag	accggccacc	480
aggggangtc	ntttncagt	gatctgcca	anantaccn	tatcatcnnt	gaataaaaag	540
gccctgaac	ganatgcttc	cancancctt	taagacccat	aatcctngaa	ccatgggtgcc	600
cttccggtct	gatccnaaag	gaatgttcct	gggtcccant	ccctcctttg	ttnccttacgt	660
tgtnttgac	ccntgctnng	atnaccnaan	tganatcccc	ngaagcacc	tnccctggc	720
atttganttt	cntaaattct	ctgcctacn	nctgaaagca	cnattccctn	ggcnccnaan	780
ggngaactca	agaaggctcn	ngaaaaacca	cncn			814

<210> 37  
 <211> 760  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(760)  
 <223> n = A,T,C or G

<400> 37						
gcattgtgct	cttccctcaa	gttggttctg	ttgccataac	aaccaccata	ggtaaagcgg	60
gcgcagtgt	cgctgaagg	gttgtagtac	cagcgcgga	tgctctcctt	gcagagtcct	120
gtgtctggca	ggctccacg	atgccctttg	tcactgggga	aatggatg	ctggagctcg	180
tcnaanccac	tcgtgtattt	ttcacangca	gcctcctccg	aagcntccg	gcagttgggg	240
gtgtcgtcac	actccactaa	actgtcgatn	cancagccca	ttgctgcagc	ggaactgggt	300
gggctgacag	gtgccagAAC	acactggatn	ggcctttcca	tggaagggcc	tggggggaaat	360
cncctnancc	caaactgcct	ctcaaaggcc	accttgacac	ccccgacagg	ctagaaatgc	420
actcttcttc	ccaaaggtag	ttgttcttgt	tgcccaagca	ncctccanca	aaccaaanc	480
ttgcaaaatc	tgctccgtgg	gggtcatnnn	taccanggtt	ggggaaanaa	acccggcngn	540
ganccnctt	gtttgaatgc	naaggnaata	atcctcctgt	cttgcttggg	tggaanagca	600
caattgaact	gttaacnttg	ggccgngttc	cncnnggtg	gtctgaaact	aatcaccgtc	660
actggaaaaa	ggtangtgcc	ttccttgaat	tcccaaantt	cccctngntt	tggtntnttt	720
ctcctctncc	ctaaaaatcg	ntttcccccc	centanggcg			760

<210> 38  
 <211> 724  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(724)  
 <223> n = A,T,C or G

<400> 38						
tttttttttt	tttttttttt	tttttttttt	tttttaaaaa	ccccctccat	tgaatgaaaa	60
cttcnnaaat	tgccaacccc	cctcnnccaa	atnnccattt	ccgggggggg	gttccaaacc	120
caaatataat	ttgganttta	aattaaatnt	tnattngggg	anaanaacaa	atgtnaagaa	180
aatttaaccc	attatnaact	taaatncctn	gaaaccctng	gnntccaaaa	atttttaacc	240
cttaaatccc	tccgaaattg	ntaanggaaa	accaaattcn	cctaaggctn	tttgaagggt	300
ngatttaaac	ccccttnant	tnnttnnacc	cnngnctnaa	ntatttngnt	tccgggtgtt	360
tcctnttaan	cntnggtaac	tcccngtaat	gaannnccct	aanccaatta	aaccgaattt	420
tttttgaatt	ggaaattccn	ngggaattna	ccgggggttt	tccnttttgg	gggccatncc	480
ccncttttgc	gggtttgggn	ntaggttgaa	tttttnnang	ncccaaaaaa	ncccccaana	540
aaaaaactcc	caagnnttaa	ttngaattnc	ccccctccca	ggccttttgg	gaaaggnggg	600
ttnttggggg	ccngggantt	cnttcccccn	ttncncccc	ccccccnggt	aaanggttat	660

ngnntttggt ttttgggccc cttnanggac cttccggatn gaaattaaat ccccggnncg 720  
gccg 724

<210> 39  
<211> 751  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(751)  
<223> n = A,T,C or G

<400> 39  
tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca 60  
caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt 120  
tttatttatt tttactgaaa gtgagaggga acttttgttg ccttttttcc tttttctgta 180  
ggccgcctta agcttttctaa atttggaaaca tctaagcaag ctgaanggaa aaggggggtt 240  
cgcaaaatca ctcggggggaa nggaaagggtt gctttgttaa tcatgcccta tgggtgggtga 300  
ttaactgctt gtacaattac ntttcacttt taattaattg tgctnaangc tttaattana 360  
cttgggggtt ccctcccccac accaaccctc ctgacaaaaa gtgccngccc tcaaatanatg 420  
tcccggnnt ctttgaaaca cacngcngaa ngttctcatt ntcccnccnc caggtnaaaa 480  
tgaagggtta ccatntttta cncacactcc acntggcnnn gcctgaatcc tcnaaaancn 540  
ccctcaancn aattnctnng ccccggtcnc gentnngtcc cncccgggtt ccgggaantn 600  
caccnccnga annnntnnc naacnaaatt ccgaaaatat tcccnntcnc tcaattcccc 660  
cnnagactnt cctcnncnan cncaattttc ttttnntcac gaacncgnnc cnnaaatgn 720  
nnnncnctc cnetngtccn naatcnccan c 751

<210> 40  
<211> 753  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(753)  
<223> n = A,T,C or G

<400> 40  
gtggtatttt ctgtaagatc aggtgttctt ccctcgtagg ttttagaggaa acaccctcat 60  
agatgaaaac ccccccagaga cagcagcact gcaactgcc aagcagccggg gtaggagggg 120  
cgccctatgc acagctgggc ccttgagaca gcagggttc gatgtcaggc tcgatgtcaa 180  
tggtctggaa gcggcggtg tacctgcgta ggggcacacc gtcaggggccc accaggaact 240  
tctcaaagtt ccaggcaacn tcgttgcgac acaccggaga ccaggtgatn agcttgggtt 300  
cggtcataan cgcggtggcg tcgtcgctgg gagctggcag ggcctcccgc aggaaggcna 360  
ataaaagggt cgccccgca ccgttcantc cgcaattctc naanaccatg angttgggtt 420  
cnaaccacc accannccgg acttccttga nggaattccc aaatctcttc gntcttgggc 480  
ttctnctgat gccctantcgt gttgcccnng atgccaanca nccccancc ccggggtcct 540  
aaanccccc cctcctcntt tcatctgggt tntntcccc ggaccntggt tcctctcaag 600  
ggancccata tctcnaccan tactcacnt nccccccnt gnnaccanc cttctanngn 660  
ttccncccc ncctctggcc cntcaanan gcttnacna cctgggtctg ccttcccccc 720  
tnccctatct gnaccnccn tttgtctcan tnt 753

<210> 41  
<211> 341  
<212> DNA  
<213> Homo sapien

<400> 41  
actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaagt 60  
agtgaacca tccttgattt atatacatat atgttctcag tattttggga gcctttccac 120  
ttctttaaac cttgttcatt atgaacactg aaaaaggaa tttgtgaaga gttaaaaagt 180



tatagcttgt	ttacgtagta	agtttttgaa	gtctacattc	aatccagaca	cttagttgag	240
tggtaaactg	tgatttttaa	aaaatatcat	ttgagaatat	tctttcagag	gtattttcat	300
ttttactttt	tgattaattg	tgttttatat	attagggtag	t		341

<210> 42  
 <211> 101  
 <212> DNA  
 <213> Homo sapien

<400> 42						
acttactgaa	tttagttctg	tgctcttcct	tatttagtgt	tgtatcataa	atactttgat	60
gtttcaaaca	ttctaaataa	ataattttca	gtggcttcat	a		101

<210> 43  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 43						
acatctttgt	tacagtctaa	gatgtgttct	taaatcacca	ttccttcctg	gtcctcacc	60
tccagggtgg	tctcacactg	taattagagc	tattgaggag	tctttacagc	aaattaagat	120
tcagatgcct	tgctaagtct	agagttctag	agttatgttt	cagaaagtct	aagaaaccca	180
cctcttgaga	ggtcagtaaa	gaggacttaa	tatttcatat	ctacaaaatg	accacaggat	240
tggtacaga	acgagagtta	tcctggataa	ctcagagctg	agtacctgcc	cgggggccgc	300
tcgaa						305

<210> 44  
 <211> 852  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(852)  
 <223> n = A,T,C or G

<400> 44						
acataaaat	cagagaaaag	tagtctttga	aatattttacg	tccaggagtt	ctttgtttct	60
gattatttgg	tgtgtgtttt	ggtttgtgtc	caaagtattg	gcagcttcag	ttttcatttt	120
ctctccatcc	tcgggcattc	ttcccaaatt	tatataccag	tcttcgtcca	tccacacgct	180
ccagaatttc	tctttttag	taatatctca	tagctcggct	gagcttttca	taggtcatgc	240
tgctgttgtt	cttcttttta	ccccatagct	gagccactgc	ctctgatttc	aagaacctga	300
agacgccctc	agatcggctc	tcccatttta	ttaatcctgg	gttcttgtct	gggttcaaga	360
ggatgtcgcg	gatgaattcc	cataagttag	tccctctcgg	gttgtgcttt	ttggtgtggc	420
acttgccagg	gggttcttgc	tcctttttca	tatcagggtga	ctctgcaaca	ggaagggtgac	480
tggtggttgt	catggagatc	tgagcccggc	agaaagtttt	gctgtccaac	aaatctactg	540
tgctaccata	gttggtgtca	tataaatagt	tctngtcttt	ccagggtgtc	atgatggaag	600
gctcagtttg	ttcagtcctg	acaatgacat	tgtgtgtgga	ctggaacagg	tcactactgc	660
actggccggt	ccacttcaga	tgctgcaagt	tgctgtagag	gagntgcccc	gccgtccctg	720
ccgcccgggt	gaactcctgc	aaactcatgc	tgcaaagggtg	ctcgccgttg	atgtcgaact	780
cntggaaagg	gatacaattg	gcatccagct	ggttggtgtc	caggaggtga	tggaagccact	840
cccacacctg	gt					852

<210> 45  
 <211> 234  
 <212> DNA  
 <213> Homo sapien

<400> 45						
acaacagacc	cttgctcgct	aacgacctca	tgctcatcaa	gttggaagaa	tccgtgtccg	60
agtctgacac	catccggagc	atcagcattg	cttcgcagtg	ccctaccgcg	gggaactctt	120
gcctcgtttc	tggtgggggt	ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	180

tgaacgtgtc ggtgggtgtct gaggaggtct gcagtaagct ctatgacccg ctgt 234

<210> 46  
 <211> 590  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(590)  
 <223> n = A,T,C or G

<400> 46  
 actttttatt taaatgttta taaggcagat ctatgagaat gatagaaaac atggtgtgta 60  
 atttgatagc aatatttttg agattacaga gtttttagtaa ttaccaatta cacagttaaa 120  
 aagaagataa tatattccaa gcanatacaa aatatctaata gaaagatcaa ggcaggaaaa 180  
 tgantataac taattgacaa tggaaaaatca attttaatgt gaattgcaca ttatccttta 240  
 aaagctttca aaanaanaaa ttattgcagt ctanttaatt caaacagtgt taaatgggtat 300  
 caggataaan aactgaaggg canaaagaat taattttcac ttcatgtaac ncacccanat 360  
 ttacaatggc ttaaattgcan ggaaaaagca gtggaagtag ggaagtantc aaggtctttc 420  
 tggctctctaa tctgccttac tctttgggtg tggtttgat cctctggaga cagctgccag 480  
 ggctcctgtt atatccacaa tcccagcagc aagatgaagg gatgaaaaag gacacatgct 540  
 gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt 590

<210> 47  
 <211> 774  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(774)  
 <223> n = A,T,C or G

<400> 47  
 acaagggggc ataatgaagg agtgggggana gatttttaag aaggaaaaaa aacgaggccc 60  
 tgaacagaat tttcctgnac aacggggcct caaaataatt ttcttgggga ggttcaagac 120  
 gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg 180  
 cattacagac gggactctgg gaggaaggat aaacagaaaag gggacaaaag ctaatcccaa 240  
 aacatcaaag aaaggaagggt ggcgtcatac ctcccagcct acacagtctt ccagggtctt 300  
 cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctctgtgtgtg 360  
 ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgtgtgat cctgcgtggc 420  
 ccacactcct tgaacacaca tcccaggtt atattccttg acatggctga acctcctatt 480  
 cctacttccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc 540  
 acggcatggg aagcctttct gacttgcttg attactccag catcttgga caatccctga 600  
 ttccccactc cttagaggca agataggggtg gtttaagagta gggctggacc acttgagacc 660  
 aggtgctggtg cttcaaattt tggctcattt acgagctatg ggaccttggg caagtnatct 720  
 tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt 774

<210> 48  
 <211> 124  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(124)  
 <223> n = A,T,C or G

<400> 48  
 canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt 60  
 ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact 120

tggt 124

<210> 49  
 <211> 147  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(147)  
 <223> n = A,T,C or G

<400> 49  
 gccgatgcta ctatttttatt gcaggaggtg ggggtgtttt tattattctc tcaacagctt 60  
 tgtggctaca ggtggtgtct gactgcatna aaaanttttt tacgggtgat tgcaaaaatt 120  
 ttagggcacc catatcccaa gcantgt 147

<210> 50  
 <211> 107  
 <212> DNA  
 <213> Homo sapien

<400> 50  
 acattaaatt aataaaaagga ctgttggggt tctgctaaaa cacatggctt gatattttgc 60  
 atggtttgag gttaggagga gttaggcata tgttttggga gaggggt 107

<210> 51  
 <211> 204  
 <212> DNA  
 <213> Homo sapien

<400> 51  
 gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgacgg 60  
 cggaaggaa aggcagagaa gtgacaccgt cagggggaaa tgacagaaag gaaaatcaag 120  
 gccttgcaag gtcagaaaag ggactcaggg cttccaccac agccctgcc cacttgcca 180  
 cctccctttt gggaccagca atgt 204

<210> 52  
 <211> 491  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(491)  
 <223> n = A,T,C or G

<400> 52  
 acaaagataa catttatctt ataacaaaaa tttgatagtt tttaaaggta gtattgtgta 60  
 gggatatttc caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca 120  
 ccatcagaca ggttttttaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa 180  
 aaaacttctt gtatcaattt cttttgttca aaatgactga ctttaantatt tttaaattatt 240  
 tcanaaacac ttctcaaaa attttcaana tggtagcttt canatgtgcc ctcagtccca 300  
 atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc 360  
 atgcaacagt gtcttttctt tnccttttct ttttttttt ttacaggcac agaaactcat 420  
 caattttatt tggataacaa aggggtctcca aatttatattg aaaaataaat ccaagttaat 480  
 atcactcttg t 491

<210> 53  
 <211> 484  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(484)  
 <223> n = A,T,C or G

<400> 53  
 acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga 60  
 gtattaacag ttgctgaagt ttgggtatttt tatgcagcat tttctttttg ctttgataac 120  
 actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct 180  
 caatcaaadc tctacataac actatagtaa ttaaaacgtt aaaaaaaagt gttgaaatct 240  
 gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc 300  
 agcttttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttggt gcctctccct 360  
 aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncg 420  
 tancttgant ctgtgtattc caggancagg cggatggaat gggccagccc ncggatgttc 480  
 cant 484

<210> 54  
 <211> 151  
 <212> DNA  
 <213> Homo sapien

<400> 54  
 actaaacctc gtgcttgatga actccatata gaaaacgggtg ccatccctga acacggctgg 60  
 ccactgggta tactgctgac aaccgcaaca acaaaaacac aaatccttgg cactggctag 120  
 tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55  
 <211> 91  
 <212> DNA  
 <213> Homo sapien

<400> 55  
 acctggcttg tctccgggtg gttcccggcg cccccacgg tccccagaac ggacactttc 60  
 gccctccagt ggatactcga gccaaagtgg t 91

<210> 56  
 <211> 133  
 <212> DNA  
 <213> Homo sapien

<400> 56  
 ggcggtatgt cgttgggtat atacaaatat gtcattttat gtaagggtact tgagtatact 60  
 tggatttttg gtatctgtgg gttgggggga cggccagga accaatatcc catggatacc 120  
 aagggacaac tgt 133

<210> 57  
 <211> 147  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(147)  
 <223> n = A,T,C or G

<400> 57  
 actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60  
 gactgggagc tgagcccttc ctttgccgcc tgctcagag gattgttgcc gacntgcana 120  
 tctcantggg ctggatncat gcagggt 147

<210> 58

<211> 198  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(198)  
 <223> n = A,T,C or G

<400> 58  
 acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60  
 tgattacata catttatcct ttaaaaaaga tgtaaatcct aatttttatg ccatctatta 120  
 attaccaat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180  
 ttgacttcta agtttggt 198

<210> 59  
 <211> 330  
 <212> DNA  
 <213> Homo sapien

<400> 59  
 acaacaaatg ggttgtagg aagtcttacc agcaaaaactg gtgatggcta ctgaaaagat 60  
 ccattgaaaa ttatcattaa tgattttaaa tgacaagtta tcaaaaactc actcaatttt 120  
 cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa 180  
 tacagtcaat aaatgacaaa gccaggcct acaggtggtt tccagacttt ccagaccag 240  
 cagaaggaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt 300  
 tttcgtcttt attggacttc tttgaagagt 330

<210> 60  
 <211> 175  
 <212> DNA  
 <213> Homo sapien

<400> 60  
 accgtgggtg cttctacat tcctgacggc tccttcacca acatctggtt ctacttcggc 60  
 gtcgtgggtc cttcctctt catcctcatc cagctggtgc tgctcatcga ctttgcgac 120  
 tcctggaacc agcgggtggt gggcaaggcc gaggagtgcg attcccgtgc ctggt 175

<210> 61  
 <211> 154  
 <212> DNA  
 <213> Homo sapien

<400> 61  
 accccacttt tcctcctgtg agcagtctgg acttctcact gctacatgat gagggtagt 60  
 gggtgtgtgt cttcaacagt atcctcccct ttccggatct gctgagccgg acagcagtgc 120  
 tggactgcac agccccggg ctccacattg ctgt 154

<210> 62  
 <211> 30  
 <212> DNA  
 <213> Homo sapien

<400> 62  
 cgctcgagcc ctatagttag tcgtattaga 30

<210> 63  
 <211> 89  
 <212> DNA  
 <213> Homo sapien

<400> 63

acaagtcatt tcagcaccct ttgctcttca aaactgacca tcttttatat ttaatgcttc 60  
ctgtatgaat aaaaatgggt atgtcaagt 89

<210> 64  
<211> 97  
<212> DNA  
<213> Homo sapien

<400> 64  
accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag 60  
aatcagtgca tccaggattg gtccttggat ctgggggt 97

<210> 65  
<211> 377  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc feature  
<222> (1) ... (377)  
<223> n = A, T, C or G

<400> 65  
acaacaanaa ntcccttctt taggccactg atggaaacct ggaacccctt tttgatggca 60  
gcatggcgtc ctaggccttg acacagcggc tggggtttgg gctntcccaa accgcacacc 120  
ccaaccctgg tctaccaca nttctggcta tgggctgtct ctgccactga acatcagggg 180  
tcggtcataa natgaaatcc caanggggac agaggtcagt agaggaagct caatgagaaa 240  
ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaaccgg 300  
tgggggtgaa ctaccccan gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360  
gggcgggagg agcatgt 377

<210> 66  
<211> 305  
<212> DNA  
<213> Homo sapien

<400> 66  
acgcctttcc ctcagaattc agggaagaga ctgtcgcttg ccttcctccg ttgttgctg 60  
agaaccctgt tgccccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120  
aggaactaac tgcaccctgg tctctctccc agtccccagt tcaccctcca tccctcacct 180  
tctccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt 240  
ttatatattt tttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300  
tggtt 305

<210> 67  
<211> 385  
<212> DNA  
<213> Homo sapien

<400> 67  
actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60  
ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcaggt ctgagagttc 120  
cccttttaaa aaagggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180  
tgtgctgtgc tggagattca cttttgagag agttctctc tgagacctga tctttagagg 240  
ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300  
cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac 360  
catagtttct gtgctagtgg accgt 385

<210> 68  
<211> 73  
<212> DNA  
<213> Homo sapien

<400> 68  
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60  
 gtttttttaa tgg 73

<210> 69  
 <211> 536  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(536)  
 <223> n = A,T,C or G

<400> 69  
 actagtccag tgtggtggaa ttccattgtg ttgggggctc tcaccctcct ctctgcagc 60  
 tccagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120  
 cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180  
 cccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240  
 cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgcgggt 300  
 actaagagcc aggcaacaga ccgttggggg ggtgaattac ttcttcgacg tagaggtggg 360  
 ccgaaccata tgtaccaagt cccagcccaa cttggacacc tgtgccttcc atgaacagcc 420  
 agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagttccct ggggagaaca 480  
 gaangtcctt gggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70  
 <211> 477  
 <212> DNA  
 <213> Homo sapien

<400> 70  
 atgaccccta acagggggcc tctcagccct cctaattgacc tccggcctag ccatgtgatt 60  
 tcacttccac tccataacgc tcttcatact aggctacta accaaccacac taaccatata 120  
 ccaatgatgg cgcgatgtaa cacgagaaag cacataccaa ggccaccaca caccacctgt 180  
 ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagtgt ttttcttcgc 240  
 agggattttt ctgagccttt taccactcca gcctagcccc taccctccaa ctaggagggc 300  
 actggccccc aacaggcatc acccgcgtaa atcccctaga agtcccactc ctaaacacat 360  
 ccgtattact cgcatacagga gtatcaatca cctgagctca ccatagtcta atagaaaaca 420  
 accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctatttt 477

<210> 71  
 <211> 533  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(533)  
 <223> n = A,T,C or G

<400> 71  
 agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact 60  
 aggtattaat agatatgtaa agaaagaaat cacaccatta ataatggtaa gattgggtta 120  
 tgtgatttta gtggtatttt tggcaccctt atatattgtt tccaaacttt cagcagtgat 180  
 attatttcca taacttaaaa agtgagtgtg aaaaagaaaa tctccagcaa gcatctcatt 240  
 taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttta aaaagctgtc 300  
 aaatagggtgt gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360  
 agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg 420  
 cttcgtaatt ttggagtang aggttccctc ctcaattttg tattttttaa aagtacatgg 480  
 taaaaaaaaa aattcacaa agtatataag gctgtaaaaat gaagaattct gcc 533

<210> 72

<211> 511  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(511)  
 <223> n = A,T,C or G

<400> 72  
 tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta 60  
 aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa 120  
 aagccgcagg atgtctacac tatancaggc gctatttggg ttggctggag gagctgtgga 180  
 aaacatggan agattgggtgc tgganacgc cgtggctatt cctcattgtt attacanagt 240  
 gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300  
 cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac 360  
 gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgcccc gtctgttatg 420  
 atttctctcc attgcagcna naaaccggtt cttctaagca aacncagggtg atgatggcna 480  
 aaatacacc cctcttgaag naccnggagg a 511

<210> 73  
 <211> 499  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(499)  
 <223> n = A,T,C or G

<400> 73  
 cagtgccagc actggtgccg gtaccagtac caataacagt gccagtgccg gtgccagcac 60  
 cagtgtggc ttcagtgtg gtgccagcct gaccgccact ctacatttg ggctcttcgc 120  
 tggccttggg ggagctggg ccagcaccag tggcagctct ggtgcctgtg gtttctccta 180  
 caagtgaat tttagatatt gttaatcctg ccagtcttct tcttcaagcc aggggtgcac 240  
 ctgagaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca 300  
 ctctgcatta aatctatttg ccatttctga aaaaaaaaaa aaaaaaagg cggccgctcg 360  
 antctagagg gcccgtttaa acccgctgat cagcctcgac tgtgccttct anttgccagc 420  
 catctgttgt ttgccctcc cccngtgcct tccttgaccc tggaaagtgc cactcccact 480  
 gtcctttcct aantaaaaat 499

<210> 74  
 <211> 537  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(537)  
 <223> n = A,T,C or G

<400> 74  
 tttcatagga gaacacactg aggagatact tgaagaatth ggattcagcc gcgaagagat 60  
 ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctctaact 120  
 tccaggccca cggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa 180  
 cattgtatgc atggaaacat ggaggaaacag tattacagtg tcctaccact ctaatcaaga 240  
 aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag 300  
 ggcttttgat ttataaanact ttgggtactt atactaaatt atggtagtta tactgccttc 360  
 cagtttgctt gatataattg ttgatattaa gattcttgac ttatatattg aatgggttct 420  
 actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat 480  
 tctacaatgt agaaatgaa ggaaatgccc caaattgtat ggtgataaaa gtcccggt 537



<210> 75  
 <211> 467  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(467)  
 <223> n = A,T,C or G

<400> 75  
 caaanacaat tgttcaaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60  
 tgcattattac acgtacctcc tcctgctcct caagtagtgt ggtctatctt gccatcatca 120  
 cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180  
 tggcacaagg aggccatctt ttccctcatcg gttattgtcc ctagaagcgt cttctgagga 240  
 tctagtggg ctttctttct gggtttgggc catttcantt ctcagtgtg tactattcta 300  
 tcattattgt ataacggtt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360  
 caatgaggaa tagccacggt gatctccagc accaaatctc tccatgttnt tccagagctc 420  
 ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tcctgn 467

<210> 76  
 <211> 400  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(400)  
 <223> n = A,T,C or G

<400> 76  
 aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctgcgcgtac 60  
 tctctctttc tggcctggag gctatccagc gtactccaaa gattcagggt tactcacgtc 120  
 atccagcaga gaatggaaag tcaaatttcc tgaattgcta tgtgtctggg ttcatccat 180  
 ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagt gagcattcag 240  
 acttgtcttt cagcaaggac tggctttct atctcttgta ctacactgaa ttcaccccca 300  
 ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360  
 ttnagtggga tcganacatg taagcagcan catgggaggt 400

<210> 77  
 <211> 248  
 <212> DNA  
 <213> Homo sapien

<400> 77  
 ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60  
 ccagctgccc cgccggggga tgcgaggctc ggagcaccct tgcccggctg tgattgctgc 120  
 caggcactgt tcatctcagc ttttctgtcc ctttgtctcc ggcaagcgt tctgtgaaa 180  
 gttcatatct ggagcctgat gtcttaacga ataaaggtcc catgctccac ccgaaaaaaa 240  
 aaaaaaaa 248

<210> 78  
 <211> 201  
 <212> DNA  
 <213> Homo sapien

<400> 78  
 actagtccag tgtggtggaa ttccattgtg ttgggcccaa cacaatggct acctttaaca 60  
 tcaccagac ccgcctctgc ccgtgcccc cgtgtgtgct aacgacagta tgatgcttac 120  
 tctgtactc ggaaactatt tttatgtaat taatgtatgc tttcttggtt ataatgcct 180  
 gatttaaaaa aaaaaaaaaa a 201

<210> 79  
 <211> 552  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(552)  
 <223> n = A,T,C or G

<400> 79  
 tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg 60  
 tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt 120  
 cctcttttct ctgaagatta atgaagtga aaattgaggt ggataaatac aaaaaggtag 180  
 tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt 240  
 atgcaagtta gtaattactc aggggttaact aaattacttt aatatgctgt tgaaacctact 300  
 ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga 360  
 taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta 420  
 ttcccaggaa tatgggggtc atttatgaat antaccggg anagaagttt tgantnaaac 480  
 cngttttgtt taatacgtta atatgtcctn aatnaacaag gcntgactta tttccaaaaa 540  
 aaaaaaaaaa aa 552

<210> 80  
 <211> 476  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(476)  
 <223> n = A,T,C or G

<400> 80  
 acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga 60  
 ggggaaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct 120  
 cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt 180  
 gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcacta 240  
 aggttaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac 300  
 tcttctaagt cctcttcag cctcactttg agtctcctt gggggttgat aggaantntc 360  
 tcttggttt ctcaataaaa tctctatcca tctcatgttt aatttggtag gcntaaaaat 420  
 gctgaaaaaa ttaaatgtt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa 476

<210> 81  
 <211> 232  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(232)  
 <223> n = A,T,C or G

<400> 81  
 ttttttttg tatgcntcn ctgtgnggtt attgttgctg ccaccctgga ggagcccagt 60  
 ttcttctgta tctttctttt ctggggggtc ttcttggtc tgccctcca ttcccagcct 120  
 ctcatcccca tcttgcaatt ttgctagggt tggaggcgt ttcttggtag cccctcagag 180  
 actcagtcag cgggaataag tcctaggggt ggggggtgtg gcaagccggc ct 232

<210> 82  
 <211> 383  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(383)  
 <223> n = A,T,C or G

<400> 82  
 aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc 60  
 agtaccagta ccaataacat gccagtgcc gtgccagcac cagtgggtggc ttcagtgtg 120  
 gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggg ggagctggtg 180  
 ccagcaccag tggcagctct ggtgcctgtg gtttctccta caagtgagat tttagatatt 240  
 gttaatcctg ccagtctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac 300  
 agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg 360  
 ccatttcaaa aaaaaaaaaa aaa 383

<210> 83  
 <211> 494  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(494)  
 <223> n = A,T,C or G

<400> 83  
 accgaattgg gaccgctggc ttataagcga tcatgtcctc cagtattacc tcaacgagca 60  
 gggagatcga gtctatacgc tgaagaaatt tgacccgatg ggacaacaga cctgctcagc 120  
 ccatcctgct cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa 180  
 acgcttcaag gtgctcatga cccagcaacc gcgcctgtgc ctctgagggg ccttaaaactg 240  
 atgtcttttc tgccacctgt taccctcctg agactccgta accaaaactct tcggactgtg 300  
 agccctgatg cctttttggc agccatactc tttggcntcc agtctctcgt ggcgattgat 360  
 tatgcttggtg tgaggcaatc atgggtggcat caccatnaa gggaacacat ttganttttt 420  
 tttcncatat tttaaattac naccagaata nttcagaata aatgaattga aaaactctta 480  
 aaaaaaaaaa aaaa 494

<210> 84  
 <211> 380  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(380)  
 <223> n = A,T,C or G

<400> 84  
 gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca 60  
 agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag 120  
 gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttctgg 180  
 gcacaccctc ctggggccca ggccggcacc tgcgtctccc agtatgcaa ctggctggtg 240  
 gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg 300  
 ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360  
 agcgttnccg cctcatccgg 380

<210> 85  
 <211> 481  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature

&lt;222&gt; (1)...(481)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 85

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gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc      60
tnccatcgtc atactgtagg tttgccacca cctcctgcat cttggggcgcg ctaatatcca      120
ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg      180
tgtgaaagga tctccagaag gagtgctcga tcttcccccac acttttgatg actttattga      240
gtcgattctg catgtccagc aggaggttgt accagctctc tgacagttag gtcaccagcc      300
ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggt gnagtctcac      360
ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggngaa      420
aaagaacacc tcttggaagt gctngccgct cctcgtcctt tggtggnngc gcntnccttt      480
t

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&lt;210&gt; 86

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(472)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 86

```

aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt      60
acttggaana gcaacttnaa gcctggacac tgggtattaaa attcacaata tgcaacactt      120
taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taaggggatg      180
ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct ttttttttga      240
cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcactttctt      300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg      360
atatntgagc ggaagantag cctttctact tcaccagaca caactccttt catattggga      420
tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg      472

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&lt;210&gt; 87

&lt;211&gt; 413

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(413)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 87

```

agaaaccagt atctctnaaa acaacctctc ataccttggt gacctaatTT tgtgtgcgtg      60
tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttTga aaagcttatg      120
cctctttTgt atctatatct gtgaaagtTT taatgatctg ccataatgtc ttggggacct      180
ttgtcttctg tgtTaatggT actagagaaa acacctatnt tatgagtcaa tctagtTngt      240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg      300
ggggacaaaag aaaagcnaaa ctgaacatna gaaacaattn cctggtgaga aattncataa      360
acagaaattg ggtngtatat tgaaanang catcattnaa acgttttttt ttt      413

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&lt;210&gt; 88

&lt;211&gt; 448

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(448)

&lt;223&gt; n = A,T,C or G

<400> 88  
 cgcagcgggt cctctctatc tagctccagc ctctcgctg ccccaactcc cgcgtcccgc 60  
 gtccctagccn accatggccg ggccctgcg cgcccgcgtg ctccctgctg ccacccctggc 120  
 cgtggccctg gccgtgagcc ccgcggccgg ctccagtcgc ggcaagccgc cgcgcctggg 180  
 gggaggccca tggaccccg gtggaagaag aagggtgtgcg gcgtgcaactg gactttgccg 240  
 tcggcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgctgcag gttgtgccgc 300  
 cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng 360  
 ttaccagaa ccnagccaat tngaacaatt nccctccat aacagcccct tttaaaaagg 420  
 gaancantcc tgntcttttc caaat ttt 448

<210> 89  
 <211> 463  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(463)  
 <223> n = A,T,C or G

<400> 89  
 gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca 60  
 gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc 120  
 agaggctctag gtctgcatat cagcagacag ttgtccgtg tattttgtag ccttgaagtt 180  
 ctcaagtaca agttntttct gatgcgaagt tctnattcca gtgttttagt cctttgcac 240  
 tttnatgttn agacttgccct ctntnaaatt gcttttgtnt tctgcaggta ctatctgtgg 300  
 tttacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn 360  
 aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn 420  
 aattcnnana anttcagtn tcatacaaca naacngganc ccc 463

<210> 90  
 <211> 400  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(400)  
 <223> n = A,T,C or G

<400> 90  
 agggattgaa ggtctntnt actgtcgac tgttcancca ccaactctac aagttgctgt 60  
 cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaat 120  
 tcttaccag tcacatcttc taggacctt ttggattcag ttagtataag ctcttccact 180  
 tcctttgtta agacttcac tggtaaaagtc ttaagtttg tagaaaggaa ttttaattgct 240  
 cgttctctaa caatgtcctc tccttgaagt atttggtga acaaccacc tnaagtcct 300  
 ttgtgcatcc attttaata tacttaatag ggcattggtg cactaggta aattctgcaa 360  
 gagtcatctg tctgcaaaag ttgcgttagt atatctgcca 400

<210> 91  
 <211> 480  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(480)  
 <223> n = A,T,C or G

<400> 91  
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ggctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac      120
atgcctcttt gactaccgtg tgccagtgtt ggtgattctc acacacctcc nncgcctctt      180
tgtggaaaaa ctggcacttg nctggaacta gcaagacatc acttacaatc tcaccacaga      240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt      300
tgtcaatact aaccgcgtgg tttgcctcca tcacatttgt gatctgtagc tctggatata      360
tctcctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt      420
ngatcaggtt cccatttccc agtccgaatg ttcacatggc atatnttact tcccacaaaa      480

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<210> 92

<211> 477

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 92

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atacagccca natcccacca cgaagatgct cttgttgact gagaacctga tgcggtcact      60
gggtcccgctg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcctt      120
cccacgcagg cagcagcggg gccggtcaat gaactccact cgtggcttgg ggttgacggt      180
taantgcagg aagaggctga ccacctcgcg gtccaccagg atgcccgaact gtgcgggacc      240
tgcagcgaaa ctctcgtatg gtcatgagcg ggaagcgaat gangcccagg gccttgccca      300
gaaccttccg cctgttctct ggcgtcacct gcagctgctg ccgctnacac tcggcctcgg      360
accagcggac aaacggcggt gaacagccgc acctcacgga tgcccantgt gtcgcgtctc      420
aggaacggcn ccagcgtgtc caggtcaatg tcggtgaanc ctccgcgggt aatggcg      477

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<210> 93

<211> 377

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(377)

<223> n = A,T,C or G

<400> 93

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gaacggctgg acctgcctc gcattgtgct gctggcagga ataccttggc aagcagctcc      60
agtcaggagc gccccagacc gctgccgccc gaagctaagc ctgcctctgg ccttcccctc      120
cgcctcaatg cagaaccant agtgggagca ctgtgtttag agttaagagt gaacactgtn      180
tgattttact tgggaatttc ctctgttata tagcttttcc caatgctaata ttccaaacaa      240
caacaacaaa ataacatggt tgctgtttna gttgtataaa agtangtgat tctgtatnta      300
aagaaaatat tactgttaca tatactgctt gcaanttctg tattttattgg tncctctggaa      360
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<210> 94

<211> 495

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(495)

<223> n = A,T,C or G

<400> 94

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cgagctgang cagatttccc acagtgaccc cagagccctg ggctatagtc tctgaccctc      120
ccaaggaaag accaccttct ggggacatgg gctggagggc aggacctaga ggcaccaagg      180
gaaggcccca ttccggggct gttccccgag gaggaaggga aggggctctg tgtgcccccc      240

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acgaggaana	ggccctgant	cctgggatca	nacacccctt	cacgtgtatc	cccacacaaa	300
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acacccaccc	agancancca	cccgccatgg	ggaatgtnc	caaggaatcg	cngggcaacg	420
tggactctng	tcccnaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	480
aaaaaaaaana	aaaaa					495

&lt;210&gt; 95

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(472)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 95

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tagctgtttt	gagttgattc	gcaccactgc	accacaactc	aatatgaaaa	ctatttnact	180
tatttattat	cttgtgaaaa	gtatacaatg	aaaattttgt	tcatactgta	tttatcaagt	240
atgatgaaaa	gcaatagata	tatattcttt	tattatgttn	aattatgatt	gccattatta	300
atcggcaaaa	tgtggagtgt	atgttctttt	cacagtaata	tatgcctttt	gtaacttcac	360
ttggttattt	tattgtaaat	gaattacaaa	attcttaatt	taagaaaatg	gtangttata	420
tttanttcan	taatttcttt	ccttgtttac	gttaattttg	aaaagaatgc	at	472

&lt;210&gt; 96

&lt;211&gt; 476

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(476)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 96

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agctggatac	atacngtggg	agttctataa	actcatacct	cagtgggact	naacccaaaat	300
tgtgttagtc	tcaattccta	ccacactgag	ggagcctccc	aaatcactat	attcttatct	360
gcaggtactc	ctccagaaaa	acngacaggg	caggcttgca	tgaaaaagtn	acatctgcgt	420
tacaaagtct	atcttcctca	nangtctgt	aaggaacaat	ttaatcttct	agcttt	476

&lt;210&gt; 97

&lt;211&gt; 479

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(479)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 97

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aaataatgct	gcaaaactta	tgttcttatg	caaaatggaa	cgctaataa	acacagctta	120
caatcgcaaa	tcaaaactca	caagtgtcga	tctgtttag	atttagtgta	ataagactta	180
gattgtgctc	cttcggatat	gattgtttct	canatcttgg	gcaatnttcc	ttagtcaaat	240
caggctacta	gaattctggt	attggatatn	tgagagcatg	aaatttttaa	naatacactt	300

gtgattatna aattaatcac aaatttcact tatacctgct atcagcagct agaaaaacat	360
ntnnttttta natcaaagta ttttgtgttt ggaantgttn aaatgaaatc tgaatgtggg	420
ttcnatctta ttttttcccn gacnactant tnttttttta gggncatttc tganccatc	479

<210> 98  
 <211> 461  
 <212> DNA  
 <213> Homo sapien

<400> 98	
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tgctagtcc tgctatctat tcgtactaa atgcagactg gaggggacca aaaaggggca	120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga	180
agtgattcag tttcctctac ggatgagaga ctggctcaag aatatactca tgcagcttta	240
tgaagccact ctgaacacgc tggttatcta gatgagaaca gagaaataaa gtcagaaaat	300
ttacctggag aaaagaggct ttggctgggg accatcccat tgaaccttct cttaaggact	360
ttaagaaaaa ctaccacatg ttgtgtatcc tgggtgccgc cgtttatgaa ctgaccaccc	420
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<210> 99  
 <211> 171  
 <212> DNA  
 <213> Homo sapien

<400> 99	
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cggcgctct gcgggcccga ggaggagcgg ctggcgggtg gggggagtgt gaccacccct	120
cggtgagaaa agccttctct agcgatctga gaggcgtgcc ttgggggtac c	171

<210> 100  
 <211> 269  
 <212> DNA  
 <213> Homo sapien

<400> 100	
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cgactgcgac gacggcgcg ggcacagtcg caggtgcagc gcgggcgcct ggggtcttgc	120
aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga	180
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cgagagatac gcaggtgcag gtggccgccc	269

<210> 101  
 <211> 405  
 <212> DNA  
 <213> Homo sapien

<400> 101	
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agtgggtgca cctccctgt agaacctggt tacaaagctt ggggcagttc acctggtctg	240
tgacctcat tttcttgaca tcaatgttat tagaagtcag gatattcttt agagagtcca	300
ctgttctgga gggagattag ggtttcttgc caaatccaac aaaatccact gaaaaagtgt	360
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<210> 102  
 <211> 470  
 <212> DNA  
 <213> Homo sapien

<400> 102	
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atatacttct	ttcagcaaac	ttgttacata	aattaaaaaa	atataacgg	ctgggtgtttt	240
caaagtacaa	ttatcttaac	actgcaaaaca	ttttaaggaa	ctaaaataaa	aaaaaacact	300
ccgcaaaggt	taaagggaac	aacaaattct	tttacaacac	cattataaaa	atcatatctc	360
aaatcttagg	ggaatatata	cttcacacgg	gatcttaact	tttactcact	ttgtttattt	420
ttttaaacca	ttgtttgggc	ccaacacaat	ggaatcccc	ctggactagt		470

&lt;210&gt; 103

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 103

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttgggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaagtga	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgccataaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
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gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
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acgttaataa	aatagcattt	tgtgaagcca	gctcaaaaga	aggcttagat	ccttttatgt	480
ccatttttagt	cactaaacga	tatcaaagtg	ccagaatgca	aaaggtttgt	gaacatttat	540
tcaaaagcta	atataagata	tttcacatac	tcatctttct	g		581

&lt;210&gt; 104

&lt;211&gt; 578

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 104

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&lt;210&gt; 105

&lt;211&gt; 538

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 105

tttttttttt	tttttcagta	ataatcagaa	caatattht	ttttatattt	aaaattcata	60
gaaaagtgcc	ttacatttaa	taaaagttht	tttctcaaa	tgatcagagg	aattagatat	120
gtcttgaaca	ccaattataa	tttgaggaaa	atacaccaaa	atacattaag	taaattattt	180
aagatcatag	agcttgtaag	tgaaaagata	aaatttgacc	tcagaaactc	tgagcattaa	240
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&lt;210&gt; 106

&lt;211&gt; 473

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 106

tttttttttt	tttttttagtc	aagtttctat	ttttattata	attaaagtct	tggtcatttc	60
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tttataaatg	taaggtgccca	ttattgagta	atatattcct	ccaagagtgg	atgtgtccct	180
tctcccacca	actaatgaac	agcaacatta	gtttaatttt	attagtagat	atacactgct	240
gcaaacgcta	attctcttct	ccatcccat	gtgatattgt	gtatatgtgt	gagttggtag	300
aatgcatcac	aatctacaat	caacagcaag	atgaagctag	gctgggcttt	cggtgaaaat	360
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ccgcttcctc	aaaggcgctg	ccacatttgt	ggctctttgc	acttgtttca	aaa	473

&lt;210&gt; 107

&lt;211&gt; 1621

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 107

cgccatggca	ctgcagggca	tctcggtcac	ggagctgtcc	ggcctggccc	cgggcccgtt	60
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a						1621

&lt;210&gt; 108

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 108

Met	Ala	Leu	Gln	Gly	Ile	Ser	Val	Met	Glu	Leu	Ser	Gly	Leu	Ala	Pro
1				5					10					15	
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			20					25					30		
Arg	Val	Asp	Arg	Pro	Gly	Ser	Arg	Tyr	Asp	Val	Ser	Arg	Leu	Gly	Arg
			35				40					45			
Gly	Lys	Arg	Ser	Leu	Val	Leu	Asp	Leu	Lys	Gln	Pro	Arg	Gly	Ala	Ala
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65					70					75					80

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<210> 109
<211> 1524
<212> DNA
<213> Homo sapien
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<400> 109

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cagaggaaaa	aaaaaaaaaa	aaaa				1524

&lt;210&gt; 110

&lt;211&gt; 3410

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 110

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<210> 111
<211> 1289
<212> DNA
<213> Homo sapien

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```

<400> 111
agccaggcgt ccctctgcct gccactcag ttggcaacacc cgggagctgt tttgtccttt 60
gtggagcctc agcagttccc tctttcagaa ctactgccca agagccctga acaggagcca 120
ccatgcagtg cttcagcttc attaaagacca tgatgatcct cttcaatttg ctcatctttc 180
tgtgtggtgc agccctggtg gcagtgggca tctgggtgtc aatcgaatgg gcaccccttc 240
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tcatcgcagc cggcgttggt gtctttgtct ttgggttccct gggctgctat ggtgctaaga 360
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gcttcaatca gcttttgtat gacatccgaa ctaatgcagt caccgtgggt ggtgtggcag 780
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aagtgaatc agcagagcct ctgggtggtg gtgtagaagg cacttcaaaa tgcataaacc 1260
tgttacaatg ttaaaaaaaaa aaaaaaaaaa 1289

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<210> 112
<211> 315
<212> PRT
<213> Homo sapien

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```

<400> 112
Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1 5 10 15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20 25 30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35 40 45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50 55 60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65 70 75 80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85 90 95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100 105 110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe

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      115      120      125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130      135      140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145      150      155
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165      170      175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
180      185      190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
195      200      205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
210      215      220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
225      230      235
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
245      250      255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
260      265      270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
275      280      285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
290      295      300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
305      310      315

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<210> 113
<211> 553
<212> PRT
<213> Homo sapien

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      <400> 113
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
1      5      10
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
20      25      30
Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val
35      40      45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
50      55      60
Leu Val Cys Val Pro Leu Gly Ser Ala Ser Asp His Trp Arg Gly
65      70      75
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
85      90      95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
100      105      110
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
115      120      125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
130      135      140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
145      150      155
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
165      170      175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
180      185      190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
195      200      205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
210      215      220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
225      230      235      240

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Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
 245 250 255  
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
 260 265 270  
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
 275 280 285  
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
 290 295 300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400  
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 435 440 445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460  
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 515 520 525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
 530 535 540  
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 545 550

<210> 114  
 <211> 241  
 <212> PRT  
 <213> Homo sapien

<400> 114  
 Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
 20 25 30  
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
 35 40 45  
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
 50 55 60  
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
 65 70 75 80  
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile  
 85 90 95  
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr  
 100 105 110  
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys

115	120	125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met		
130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		
165	170	175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		
180	185	190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		
195	200	205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		
210	215	220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu		
225	230	235
Gln		240

<210> 115  
 <211> 366  
 <212> DNA  
 <213> Homo sapien

<400> 115  
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 catttcactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac 120  
 ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180  
 actggtagaa aaacatctga agagctagtc tatcagcatc tgacaggtga attggatggt 240  
 tctcagaacc atttcacca gacagcctgt ttctatcctg tttaataaat tagtttgggt 300  
 tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt 360  
 ttagtc 366

<210> 116  
 <211> 282  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(282)  
 <223> n = A,T,C or G

<400> 116  
 acaaagatga accatttcct atattatagc aaaattaaaa tctacccgta ttctaattatt 60  
 gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa 120  
 agactttact attttcatat tttaagacac atgatttatc ctattttagt aacctggttc 180  
 atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt 240  
 tcaatctnga actatctana tcacagacat ttctattcct tt 282

<210> 117  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(305)  
 <223> n = A,T,C or G

<400> 117  
 acacatgtcg cttcactgcc ttcttagatg cttctgggtca acatanagga acagggacca 60  
 tattttatcct ccctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120



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aataaggcaa aatatatgaa acaacaggtc tcgagatatt ggaaatcagt caatgaagga      180
tactgatccc tgatcactgt cctaattgcag gatgtgggaa acagatgagg tcacctctgt      240
gactgcccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat      300
tggtt                                           305

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<210> 118
<211> 71
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(71)
<223> n = A,T,C or G

```

```

<400> 118
accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa      60
aantcctggg t                                           71

```

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<210> 119
<211> 212
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(212)
<223> n = A,T,C or G

```

```

<400> 119
actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca      60
gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac      120
agtaagctgg cccttctaataaaaagaaaat tgaaagggtt ctcactaanc ggaattaant      180
aatggantca aganactccc aggcctcagc gt                                           212

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<210> 120
<211> 90
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(90)
<223> n = A,T,C or G

```

```

<400> 120
actcgttgca natcaggggc ccccagagt caccgttgca ggagtccttc tggctctggc      60
ctccgccggc gcagaacatg ctggggtggt                                           90

```

```

<210> 121
<211> 218
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(218)
<223> n = A,T,C or G

```

```

<400> 121
tgtancgtga anacgcacaga naggggtgtc aaaaatggag aanccttgaa gtcattttga      60
gaataagatt tgctaaaaga tttggggcta aaacatggtt attgggagac atttctgaag      120

```

atatncangt aaattangga atgaattcat ggttcttttg ggaattcctt tacgatngcc 180  
agcatanact tcatgtgggg atancagcta cccttgta 218

<210> 122  
<211> 171  
<212> DNA  
<213> Homo sapien

<400> 122  
taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg 60  
catttgtag ctcatggaac aggaagtcgg atgggtggggc atcttcagtg ctgcatgagt 120  
caccaccccg gcgggggtcat ctgtgccaca ggtccctggt gacagtgcgg t 171

<210> 123  
<211> 76  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(76)  
<223> n = A,T,C or G

<400> 123  
tgtagcgtga agacnacaga atgggtgtgtg ctgtgctatc caggaacaca tttattatca 60  
ttatcaanta ttgtgt 76

<210> 124  
<211> 131  
<212> DNA  
<213> Homo sapien

<400> 124  
acctttcccc aaggccaatg tcctgtgtgc taactggccg gctgcaggac agctgcaatt 60  
caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg 120  
ttaagatttg t 131

<210> 125  
<211> 432  
<212> DNA  
<213> Homo sapien

<400> 125  
actttatcta ctggctatga aatagatggt ggaaaattgc gttaccaact ataccactgg 60  
cttgaaaaag aggtgatagc tcttcagagg acttgtgact ttgtctcaga tgctgaagaa 120  
ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat 180  
ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg 240  
ctcttgaagt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc 300  
catggtgggg gtcttgcac tgtaagaatg gaattgattt tgcttttgca agaattctcag 360  
caggaaacat cagaaccact attttctagc cctctgtcag agcaaaccct agtgccctctc 420  
ctctttgctt gt 432

<210> 126  
<211> 112  
<212> DNA  
<213> Homo sapien

<400> 126  
acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60  
agtaagaatg atatttcccc ccagggatca ccaaatattt ataaaaattt gt 112

<210> 127

<211> 54  
<212> DNA  
<213> Homo sapien

<400> 127  
accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128  
<211> 323  
<212> DNA  
<213> Homo sapien

<400> 128  
acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc 60  
acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgtca 120  
ttctctctga agtctaggtt acccattttg gggacccatt ataggcaata aacacagttc 180  
ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcccttt tcttagcctt 240  
ttcctgcaaa aggtcactc agtcccttgc ttgtctcagt gactgggctc cccagggcct 300  
aggctgcctt cttttccatg tcc 323

<210> 129  
<211> 192  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(192)  
<223> n = A,T,C or G

<400> 129  
acatacatgt gtgtatat ttaaataatca cttttgtatc actctgactt tttagcatac 60  
tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc 120  
tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg 180  
gataaacaaa gt 192

<210> 130  
<211> 362  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(362)  
<223> n = A,T,C or G

<400> 130  
ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60  
tataatgacg caacaaaaag gtgctgttta gtcctatggg tcagtttatg cccctgacaa 120  
gtttccattg tgttttgccg atcttctggc taatcgtggg atcctccatg ttattagtaa 180  
ttctgtattc cattttgtta acgcctggta gatgtaacct gctangaggc taactttata 240  
cttattttaa agctcttatt ttgtggtcac taaaatggca atttatgtgc agcactttat 300  
tgcagcagga agcacgtgtg gggtggttgt aaagctcttt gctaattctta aaaagtaatg 360  
gg 362

<210> 131  
<211> 332  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature

&lt;222&gt; (1)...(332)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 131

ctttttgaaa gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt ttcccatgca	60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga	120
gttctcccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc	180
ttctgaacta gattaaggca gcttgtaaatt ctgatgtgat ttggttttatt atccaactaa	240
cttccatctg ttatcactgg agaaagccca gactccccan gacnggtacg gattgtgggc	300
atanaaggat tgggtgaagc tggcgttgtg gt	332

&lt;210&gt; 132

&lt;211&gt; 322

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(322)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 132

acttttgcca ttttgtatat ataaacaatc ttgggacatt ctcctgaaaa ctagggtgtcc	60
agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat	120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt	180
tttagcaagt taaaatgaan atgacaggaa aggcttattt atcaacaaag agaagagttg	240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct aggggaagcct	300
gtaacaatct acaattggtc ca	322

&lt;210&gt; 133

&lt;211&gt; 278

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(278)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 133

acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt	60
cttggttttc tttccatctg gctcctgggt tgacaatttg tggaaacaac tctattgcta	120
ctatttaaaa aaaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg	180
ctattcctgt tttgtcaaag aaattatatt tttcaaaaata tgtntatttg tttgatgggt	240
cccacgaaac actaataaaa accacagaga ccagcctg	278

&lt;210&gt; 134

&lt;211&gt; 121

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(121)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 134

gtttanaaaa ctgttttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca	60
tgattctctg aggttaaact tgggtttcaa atgttatatt tacttgtatt ttgcttttgg	120
t	121

&lt;210&gt; 135

<211> 350  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(350)  
 <223> n = A,T,C or G

<400> 135  
 acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctataacc 60  
 atancaagtg gtgactgggt aagcgtgcga caaaggctcag ctggcacatt acttgtgtgc 120  
 aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggactacca 180  
 ggggtgcccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgct 240  
 ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag 300  
 ttcccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt 350

<210> 136  
 <211> 399  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(399)  
 <223> n = A,T,C or G

<400> 136  
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60  
 gctgtgattg tatccgaata ntctcgtga gaaaagataa tgagatgacg tgagcagcct 120  
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180  
 cctggcgccc agccagccag ccacagggtg gcttcttctt tttgtgtgta caacnccaag 240  
 aaaactgcag agggccaggg tcaggtgtna gtgggtangt gaccataaaa caccagggtgc 300  
 tcccaggaaac ccgggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360  
 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137  
 <211> 165  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(165)  
 <223> n = A,T,C or G

<400> 137  
 actggtgtgg tngggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60  
 ggaggaaagt tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120  
 ttggctgtgc ccactggtgg tcactgtcat tgggtggggt cctgt 165

<210> 138  
 <211> 338  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(338)  
 <223> n = A,T,C or G

<400> 138

```

actcactgga atgccacatt cacaacagaa tcagagggtct gtgaaaacat taatggctcc      60
ttaacttttc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccac      120
tgctgggcag tctcccatgc cttccacagt gaaagggcct gagaaaaatc acatccaatg      180
tcatgtgttt ccagccacac caaaagggtgc ttgggggtgga gggctggggg catananggt      240
cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa      300
aaaaactgat gccttttttt tttttttttg taaaattc                                338

```

<210> 139

<211> 382

<212> DNA

<213> Homo sapien

<400> 139

```

gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa      60
gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccga gtgaaggaga      120
attcaaacag acctcgtcat tcttggtgtg agcctggctg gctcaccgcc tatcatctgc      180
atttgcctta ctcagggtgt accggactct ggcccctgat gtctgtagtt tcacaggatg      240
ccttattttg cttctacacc ccacagggcc ccctacttct tcggatgtgt ttttaataat      300
gtcagctatg tgcccacatc tcttccatgc cctccctccc tttcctacca ctgctgagt      360
gcctggaact tgtttaaagt gt                                382

```

<210> 140

<211> 200

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(200)

<223> n = A,T,C or G

<400> 140

```

accaaaactt ctttctgttg tgttngattt tactataggg gtttngcttn ttctaaanat      60
acttttcatt taacancttt tgtaagtgt caggctgcac ttgctccat anaattattg      120
ttttcacatt tcaacttgta tgtgtttgtc tcttanagca ttggtgaaat cacatatttt      180
atattcagca taaaggagaa                                200

```

<210> 141

<211> 335

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(335)

<223> n = A,T,C or G

<400> 141

```

actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggttg      60
gggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc agggtttgtt      120
atgcatgtag agaaccctaa ctaatttatt aaacaggata gaaacaggct gtctgggtga      180
aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg      240
tttttctacc agttcagaga tnggttaatg actantcca atggggaaaa agcaagatgg      300
attcacaac caagtaattt taacaaaga cactt                                335

```

<210> 142

<211> 459

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

&lt;222&gt; (1)...(459)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 142

accagggttaa	tattgccaca	tatataccttt	ccaattgcgg	gctaaacaga	cgtgtattta	60
gggttggtta	aagacaaccc	agcttaatat	caagagaaat	tgtgaccttt	catggagtat	120
ctgatggaga	aaacactgag	ttttgacaaa	tcttatttta	ttcagatagc	agtctgatca	180
cacatgggcc	aacaacactc	aaataataaa	tcaaatatna	tcagatgtta	aagattgggc	240
ttcaaacatc	atagccaatg	atgccccgct	tgcctataat	ctctccgaca	taaaaccaca	300
tcaacacctc	agtggccacc	aaaccattca	gcacagcttc	cttaactgtg	agctgtttga	360
agctaccagt	ctgagcacta	ttgactatnt	ttttcangct	ctgaatagct	ctagggatct	420
cagcangggg	gggaggaacc	agctcaacct	tggcgtaant			459

&lt;210&gt; 143

&lt;211&gt; 140

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 143

acatttcctt	ccaccaagtc	aggactcctg	gcttctgtgg	gagttcttat	cacctgaggg	60
aaatccaaac	agttctctct	agaaaggaat	agtgtcacca	acccacacca	tctccctgag	120
accatccgac	ttccctgtgt					140

&lt;210&gt; 144

&lt;211&gt; 164

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(164)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 144

acttcagtaa	caacatacaa	taacaacatt	aagtgtatat	tgccatcttt	gtcattttct	60
atctatacca	ctctcccttc	tgaaaacaan	aatcactanc	caatcactta	tacaaatttg	120
aggcaattaa	tccatatttg	ttttcaataa	ggaaaaaaag	atgt		164

&lt;210&gt; 145

&lt;211&gt; 303

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(303)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 145

acgtagacca	tcgaactttg	tatttgtaat	ggcaaacatc	cagnagcaat	tcctaaacaa	60
actggagggt	atttataccc	aattatccca	ttcattaaca	tgccctcctc	ctcaggctat	120
gcaggacagc	tatcataagt	cggcccaggc	atccagatac	taccatttgt	ataaacttca	180
gtaggggagt	ccatccaagt	gacaggtcta	atcaaaggag	gaaatggaac	ataagcccag	240
tagtaaaatn	ttgcttagct	gaaacagcca	caaaagactt	accgccgtgg	tgattaccat	300
caa						303

&lt;210&gt; 146

&lt;211&gt; 327

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

<221> misc\_feature  
 <222> (1)...(327)  
 <223> n = A,T,C or G

<400> 146  
 actgcagctc aattagaagt ggtctctgac ttctcatcanc ttctccctgg gctccatgac 60  
 actggcctgg agtgactcat tgctctggtt gggtgagaga gctcctttgc caacaggcct 120  
 ccaagtcagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt 180  
 cctgaacagg gaggggtggga ggagccagca tggaacaagc tgccactttc taaagtagcc 240  
 agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300  
 taggggtgag ctgtgtgact ctatggt 327

<210> 147  
 <211> 173  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(173)  
 <223> n = A,T,C or G

<400> 147  
 acattgtttt ttgagataa agcattgana gagctctcct taacgtgaca caatggaagg 60  
 actggaacac atacccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120  
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt 173

<210> 148  
 <211> 477  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(477)  
 <223> n = A,T,C or G

<400> 148  
 acaaccactt tatctcatcg aatttttaac ccaaactcac tcaactgtgcc ttctctatcct 60  
 atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120  
 gccctactac ctgctgcaat aatcacattc ccttcctgtc ctgaccctga agccattggg 180  
 gtggctctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgtctac 240  
 nccanccac ctcaccgacc ccatcctctt acacagctac ctccttgctc tctaacccca 300  
 tagattatnt ccaaattcag tcaattaagt tactattaac actctaccgg acatgtccag 360  
 caccactggg aagccttctc cagccaacac acacacacac acacncacac acacacatat 420  
 ccaggcacag gctacctcat cttcacaaac acccctttaa ttaccatgct atggtgg 477

<210> 149  
 <211> 207  
 <212> DNA  
 <213> Homo sapien

<400> 149  
 acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac 60  
 taacgtatatt tagagagcca aggaagggtt ctgtggggag tgggatgtaa ggtggggcct 120  
 gatgataaat aagagtcagc caggtaagtg ggtggtgtgg tatgggcaca gtgaagaaca 180  
 tttcaggcag agggaacagc agtgaaa 207

<210> 150  
 <211> 111  
 <212> DNA  
 <213> Homo sapien



<220>  
 <221> misc\_feature  
 <222> (1)...(111)  
 <223> n = A,T,C or G

<400> 150  
 accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg 60  
 cacttaaatg tggtcagtgt ttggacttgt taactantgg catctttggg t 111

<210> 151  
 <211> 196  
 <212> DNA  
 <213> Homo sapien

<400> 151  
 agcgcggcag gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac 60  
 agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat 120  
 ggataccaac cggaaaaccc ctatcccga cagcccactg tggccccac tgtctacgag 180  
 gtgcatccgg ctacgt 196

<210> 152  
 <211> 132  
 <212> DNA  
 <213> Homo sapien

<400> 152  
 acagcacttt cacatgtaag aaggagagaaa ttcctaaatg taggagaaag ataacagaaac 60  
 cttccctttt tcatctagtgt gtggaaacct gatgctttat gttgacagga atagaaccag 120  
 gagggagtgt gt 132

<210> 153  
 <211> 285  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(285)  
 <223> n = A,T,C or G

<400> 153  
 acaanaccca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag 60  
 cttctgctct tatgtcttca tctgacaact ctttaccatt tttatcctcg ctgagcagga 120  
 gcacatcaat aaagtccaaa gtcttggact tggccttggc ttggaggaag tcatcaacac 180  
 cctggctagt gaggggtgcg cgccgctcct ggatgacggc atctgtgaag tcgtgcacca 240  
 gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt 285

<210> 154  
 <211> 333  
 <212> DNA  
 <213> Homo sapien

<400> 154  
 accacagtcc tgttgggcca gggcttcatg accctttctg tgaaaagcca tattatcacc 60  
 accccaaatt tttccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac 120  
 cctaagccgg ttacacagct aactcccact ggccctgatt tgtgaaattg ctgctgcctg 180  
 attggcacag gagtgcgaag tgttcagctc cctcctccg tggaaacgaga ctctgatttg 240  
 agtttcacaa attctcgggc cacctcgtca ttgctcctct gaaataaaat ccggagaatg 300  
 gtcaggcctg tctcatccat atggatcttc cgg 333

<210> 155

<211> 308  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(308)  
 <223> n = A,T,C or G

<400> 155  
 actggaaata ataaaaccca catcacagtg ttgtgtcaaa gatcatcagg gcatggatgg 60  
 gaaagtgtct tgggaactgt aaagtgccta acacatgata gatgattttt gttataatat 120  
 ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggcccag cccagcccc 180  
 atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggt 240  
 gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtgta aggcattgctg 300  
 gccctggt 308

<210> 156  
 <211> 295  
 <212> DNA  
 <213> Homo sapien

<400> 156  
 acctgtctcg gtgcttgga catattagga actcaaaata tgagatgata acagtgccta 60  
 ttattgatta ctgagagaac tgtagacat ttagttgaag attttctaca caggaactga 120  
 gaataggaga ttatgtttgg cctcatatt ctctcctatc ctcttgcct cattctatgt 180  
 ctaatatatt ctcaatcaaa taaggtttagc ataatcagga aatcgaccaa ataccaatat 240  
 aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat 295

<210> 157  
 <211> 126  
 <212> DNA  
 <213> Homo sapien

<400> 157  
 acaagtttaa atagtgtgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct 60  
 gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc 120  
 cttagt 126

<210> 158  
 <211> 442  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(442)  
 <223> n = A,T,C or G

<400> 158  
 acccactggg cttggaaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg 60  
 aanccagcag gctgccccta gtcagtcctt ccttcagag aaaaagagat ttgagaaagt 120  
 gcctgggtaa ttcaccatta atttctccc ccaaactctc tgagtcttcc cttaatattt 180  
 ctggtgggtc tgaccaaaagc aggtcatggg ttgttgagca tttgggatcc cagtgaagta 240  
 natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtgg cagagtgggtg 300  
 ccaaccctgt tttccagtc cacgtagaca gattcacagt gcggaattct ggaagctgga 360  
 nacagacggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg 420  
 tgttcattct ctgatgtcct gt 442

<210> 159  
 <211> 498  
 <212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(498)

<223> n = A,T,C or G

<400> 159

acttccaggt aacgttggtg tttccgttga gcctgaactg atgggtgacg ttgtaggttc	60
tccaacaaga actgaggttg cagagcgggt aggggaagagt gctgttccag ttgcacctgg	120
gctgctgtgg actgttggtg attcctcact acggcccaag gttgtggaac tggcanaaag	180
gtgtgttggt gganttgagc tcgggcggct gtggtaggtt gtgggtctct caacaggggc	240
tgctgtggtg ccgggangtg aangtggtgt gtcacttgag cttggccagc tctggaaagt	300
antanattct tcctgaaggc cagcgcttgt ggagctggca ngggtcantg ttgtgtgtaa	360
cgaaccagtg ctgctgtggg tgggtgtana tcctccacaa agcctgaagt tatggtgtcn	420
tcaggtaana atgtggttcc agtgtccctg ggcngctgtg gaaggttgta natgtgcacc	480
aagggaataa gctgtggt	498

<210> 160

<211> 380

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(380)

<223> n = A,T,C or G

<400> 160

acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac	60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct	120
ggagcatggc atagaggaag ctganaaatg tggggtctga ggaagccatt tgagtctggc	180
cactagacat ctcacagccc acttggtgtga agagatgccc catgacccca gatgcctctc	240
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg	300
gagaaaaatg gcagtttgac cgaacctgtt cacaacggta gaggttgatt tctaacgaaa	360
cttgtagaat gaagcctgga	380

<210> 161

<211> 114

<212> DNA

<213> Homo sapien

<400> 161

actccacatc ccctctgagc aggcggttgt cgttcaaggt gtatttgccc ttgcctgtca	60
cactgtccac tggccctta tccacttggt gcttaatccc tcgaaagagc atgt	114

<210> 162

<211> 177

<212> DNA

<213> Homo sapien

<400> 162

actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa	60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt	120
tggtgatata taacttgga ataaccagc ctggtgatac ataaaactac tcactgt	177

<210> 163

<211> 137

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature  
 <222> (1)...(137)  
 <223> n = A,T,C or G

<400> 163

catttataca	gacaggcgtg	aagacattca	cgacaaaaac	gcgaaattct	atcccgtgac	60
canagaaggc	agctacggct	actcctacat	cctggcgtgg	gtggccttcg	cctgcacctt	120
catcagcggc	atgatgt					137

<210> 164  
 <211> 469  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(469)  
 <223> n = A,T,C or G

<400> 164

cttatcacia	tgaatgttct	cctgggcagc	gttgtgatct	ttgccacctt	cgtgacttta	60
tgcaatgcat	catgctatct	cataccta	gaggagattc	aaccaggaaa		120
tgcatggatc	tcaaaggaaa	caaacaccca	ataaactcgg	agtggcagac	tgacaactgt	180
gagacatgca	cttgctacga	aacagaaatt	tcatgttgca	cccttgtttc	tacacctgtg	240
ggttatgaca	aagacaactg	caaagaatc	ttcaagaagg	aggactgcaa	gtatatcgtg	300
gtggagaaga	aggacccaaa	aaagacctgt	tctgtcagtg	aatggataat	ctaagtgtct	360
tctagtaggc	acagggctcc	caggccaggc	ctcattctcc	tctggcctct	aatagtcaat	420
gattgtgtag	ccatgcctat	cagtaaaaaa	atntttgagc	aaacacttt		469

<210> 165  
 <211> 195  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(195)  
 <223> n = A,T,C or G

<400> 165

acagtttttt	atanatatcg	acattgccgg	cacttgtgtt	cagtttcata	aagctggtgg	60
atccgctgtc	atccactatt	ccttggctag	agtaaaaatt	attcttatag	cccatgtccc	120
tgcaggccgc	ccgccgtag	ttctcgctcc	agtcgtcttg	gcacacaggg	tgccaggact	180
tcctctgaga	tgagt					195

<210> 166  
 <211> 383  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(383)  
 <223> n = A,T,C or G

<400> 166

acatcttagt	agtgtggcac	atcagggggc	catcagggtc	acagtcactc	atagcctcgc	60
cgaggtcgga	gtccacacca	ccggtgtagg	tgtgtcfaat	cttgggcttg	gcgcccacct	120
ttggagaagg	gatatgtctg	acacacatgt	ccacaaagcc	tgtgaactcg	ccaaagaatt	180
tttgacagcc	agcctgagca	aggggcggat	gttcagcttc	agctcctcct	tcgtcagggtg	240
gatgccaaac	tcgtctangg	tccgtgggaa	gctgggtgtc	acntcaccta	caacctgggc	300
gangatctta	taaagaggct	ccnagataaa	ctccacgaaa	cttctctggg	agctgctagt	360

nggggccttt ttggtgaact ttc

383

<210> 167

<211> 247

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(247)

<223> n = A,T,C or G

<400> 167

acagagccag accttggcca taaatgaanc agagattaag actaaacccc aagtcganat	60
tgagagcagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc	120
tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac	180
tcaatctgan tccaaagtgg tggctggaac actggtcatg acanaggcag tgactctgac	240
tgangtc	247

<210> 168

<211> 273

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(273)

<223> n = A,T,C or G

<400> 168

acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa	60
aatccctcan ccttgttctt cactactgtc tatactgana gtgtcatgtt tccacaaagg	120
gctgacacct gagcctgnat tttcactcat ccctgagaag ccctttccag taggggtgggc	180
aattcccaac ttccttgcca caagcttccc aggctttctc ccctggaaaa ctccagcttg	240
agtcccagat aactcatgg gctgccctgg gca	273

<210> 169

<211> 431

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 169

acagccttgg cttcccaaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc	60
agctcagacc aggggtcaaag gatgtgacat caacagtttc tggtttcaga acaggttcta	120
ctactgtcaa atgacccccc atacttcctc aaaggctgtg gtaagttttg cacagggtgag	180
ggcagcagaa aggggggtant tactgatgga caccatcttc tctgtatact ccacactgac	240
cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcactgctgg gcaccagctc	300
acgcacatca ctgacaaccg gcatggaaaa agaantgcc aatttcatac atccaactgg	360
aaagtgatct gatactggat tcttaattac cttcaaaaagc ttctgggggc catcagctgc	420
tcgaacactg a	431

<210> 170

<211> 266

<212> DNA

<213> Homo sapien

<220>

55

<221> misc\_feature  
 <222> (1)...(266)  
 <223> n = A,T,C or G

<400> 170  
 acctgtgggc tgggctgtta tgcctgtgcc ggctgtgaa agggagttca gaggtggagc 60  
 tcaaggagct ctgcaggcat tttgccaanc ctctccanag canagggagc aacctacact 120  
 ccccgctaga aagacaccag attggagtc tgggagggg agttggggtg ggcatattgat 180  
 gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240  
 tcaaagctag gggctctggca ggtgga 266

<210> 171  
 <211> 1248  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(1248)  
 <223> n = A,T,C or G

<400> 171  
 ggcagccaaa tcataaacgg cgaggactgc agcccgact cgcagccctg gcaggcggca 60  
 ctggcatgag aaaacgaatt gttctgctcg ggctgctgg tgcacccgca gtgggtgctg 120  
 tcagccgcac actgtttcca gaagtgaagt cagagctcct acaccatcgg gctgggcctg 180  
 cacagtcttg aggcggacca agagccaggg agccagatgg tggaggccag cctctccgta 240  
 cggcaccagc agtacaacag acccttgctc gctaacgacc tcatgctcat caagtggac 300  
 gaatccgtgt ccgagtcga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360  
 gcggggaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420  
 gtgctgcagt gcgtgaacgt gtcggtgggt tctgaggagg tctgcagtaa gctctatgac 480  
 ccgctgtacc accccagcat gttctgcgcc ggccgagggc aagaccagaa ggactcctgc 540  
 aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtctttc 600  
 ggaaaagccc cgtgtggcca agttggcgtg ccaggtgtct acaccaacct ctgcaaattc 660  
 actgagtggg tagagaaaac cgtccaggcc agttaactct ggggactggg aacccatgaa 720  
 attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agccccctct 780  
 ccctcaggcc caggagtcca ggccccagc ccctcctccc tcaaaccaag ggtacagatc 840  
 cccagcccc cctccctcag acccaggagt ccagaccccc cagccccctc tccctcagac 900  
 ccaggagtcc agcccctcct ccctcagacc caggagtcca gacccccag cccctcctcc 960  
 ctcagaccca ggggtccagg cccccaaccc ctcctccctc agactcagag gtccaagccc 1020  
 ccaaccntc attccccaga cccagaggtc caggtccag cccctcntcc ctcagaccca 1080  
 gcggtccaat gccacctaga ctntccctgt acacagtgcc cccttggtggc acgttgacct 1140  
 aaccttacca gttggttttt catttttngt ccctttcccc tagatccaga aataaagttt 1200  
 aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1248

<210> 172  
 <211> 159  
 <212> PRT  
 <213> Homo sapien

<220>  
 <221> VARIANT  
 <222> (1)...(159)  
 <223> Xaa = Any Amino Acid

<400> 172  
 Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro  
 1 5 10 15  
 Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser  
 20 25 30  
 Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr  
 35 40 45  
 Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly

56

50	Arg Met Pro Thr Val	55	Leu Gln Cys Val Asn Val	60	Ser Val Val Ser Glu
65	Glu Val Cys Ser Lys	70	Leu Tyr Asp Pro Leu Tyr	75	His Pro Ser Met Phe
	85	90	Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser	95	
	100	105	Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe	110	
	115	120	Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn	125	
	130	135	Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser	140	
	145	150		155	

&lt;210&gt; 173

&lt;211&gt; 1265

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1265)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 173

```

ggcagccgc actgcagcc ctggcaggcg gcaactggtca tggaaaacga attgttctgc      60
tcgggcgctc tgggtgcatcc gcagtgggtg ctgtcagccg cacactgttt ccagaactcc      120
tacaccatcg ggctgggcct gcacagtctt gaggccgacc aagagccagg gagccagatg      180
gtggaggcca gcctctccgt acggcaccca gagtacaaca gaccttgct cgctaacgac      240
ctcatgctca tcaagttgga cgaatccgtg tccgagtctg acaccatccg gagcatcagc      300
attgcttcgc agtgccctac cgcggggaac tcttgccctg tttctggctg gggctctgctg      360
gcgaacggtg agctcacggg tgtgtgtctg cctcttcaa ggaggtcctc tgcccagtcg      420
cgggggctga cccagagctc tgcgtcccag gcagaatgcc taccgtgctg cagtgcgtga      480
acgtgtcggg ggtgtctgag gaggtctgca gtaagctcta tgaccgctg taccaccca      540
gcatgttctg cgccggcgga gggcaagacc agaaggactc ctgcaacggt gactctgggg      600
ggccccgat ctgcaacggg tacttgacag gccttggtgc tttcgaaaa gccccgtgtg      660
gccaaagttg cgtgccagggt gtctacacca acctctgcaa attcactgag tggatagaga      720
aaaccgtcca ggccagttaa ctctggggac tgggaaccca tgaaattgac ccccaaatac      780
atcctgcgga aggaattcag gaatatctgt tcccagcccc tcttccctca ggcccaggag      840
tccaggcccc cagccccctc tccctcaaac caagggtaca gatccccagc cctctctccc      900
tcagaccagc gagtcagac cccccagccc ctctccctc agaccagga gtccagcccc      960
tctcctntca gaccagagg tccagacccc ccagccctc ctccctcaga cccaggggtt     1020
gaggccccca accctcctc cttcagagtc agaggtccaa gcccccaacc cctcgttccc     1080
cagacccaga ggttnaggtc ccagcccctc ttccntcaga cccagnngtc caatgccacc     1140
tagattttcc ctgnacacag tgcccccttg tggngangttg acccaacctt accagttggt     1200
tttcatattt tngtcccttt cccctagatc cagaaataaa gtttaagaga nngncaaaaa     1260
aaaaa                                         1265

```

&lt;210&gt; 174

&lt;211&gt; 1459

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1459)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 174

```

ggtcagccgc aactgtttc cagaagttag tgcagagctc ctacaccatc gggctgggcc      60
tgcacagtct tgaggccgac caagagccag ggagccagat ggtggaggcc agcctctccg      120
tacggcaccc agagtacaac agacccttgc tcgtaacga cctcatgctc atcaagttgg      180

```

acgaatccgt	gtccgagtct	gacaccatcc	ggagcatcag	cattgcttcg	cagtgcccta	240
ccgcggggaa	ctcttgctc	gtttctggct	ggggtctgct	ggcgaacggt	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggtcct	ctgcccagtc	gcgggggctg	accagagct	360
ctgcgctcca	ggcagaatgc	ctaccgtgct	gcagtgcgtg	aacgtgtcgg	tggtgtctga	420
ngaggtctgc	antaagctct	atgacccgct	gtaccacccc	ancatgttct	gcgccggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcaggcgact	540
cagggaaggg	tggagaaggg	ggagacagag	acacacaggg	ccgcatggcg	agatgcagag	600
atggagagac	acacagggag	acagtgacaa	ctagagagag	aaactgagag	aaacagagaa	660
ataaacacag	gaataaagag	aagcaaagga	agagagaaac	agaaacagac	atggggaggc	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcatggggcc	tgagggcggg	780
gacctccacc	caatagaaaa	tectcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtcgattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttggg	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	ttttttaa	tggttgaact	ctcctaaaa	ttttctgatg	tgtttattga	1020
aaaaatccaa	gtataagtgg	acttgtgcat	tcaaaccagg	gttgttcaag	ggtcaactgt	1080
gtacccagag	ggaaacagtg	acacagattc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aatcaagac	tctacaaaga	ggctgggcag	ggtggctcat	gcctgtaatc	ccagcacttt	1200
gggaggcgag	gcaggcagat	cacttgaggt	aaggagttca	agaccagcct	ggccaaaatg	1260
gtgaaatcct	gtctgtacta	aaaatacaaa	agttagctgg	atatggtggc	aggcgctgt	1320
aatccagct	acttgggagg	ctgaggcagg	agaattgctt	gaatatggga	ggcagaggtt	1380
gaagtgaagt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaa					1459

&lt;210&gt; 175

&lt;211&gt; 1167

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1167)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 175

gcgcagccct	ggcaggcggc	actggtcatg	gaaaacgaat	tggtctgctc	gggcgtcctg	60
gtgcatccgc	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggg	120
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggt	ggaggccagc	180
ctctccgtac	ggcaccacaga	gtacaacaga	ctcttgctcg	ctaacgacct	catgctcatc	240
aagtggagc	aatccgtgtc	cgagtctgac	accatccgga	gcatcagcat	tgcttcgcag	300
tgccctaccg	cggggaaactc	ttgctcgtgn	tctggtggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgctgcactg	cgtgaacgtg	tcgggtggtg	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgccc	gcggagggca	agaccagaag	480
gactcctgca	acggtgactc	tggggggccc	ctgatctgca	acgggtactt	gcagggcctt	540
gtgtctttcg	gaaaagcccc	gtgtggccaa	cttggcgtgc	caggtgtcta	caccaacctc	600
tgcaaattca	ctgagtggat	agagaaaacc	gtccagncca	gttaactctg	gggactggga	660
acccatgaaa	ttgaccccca	aatacatcct	gcggaangaa	ttcaggaata	tctgttccca	720
gcccctcctc	cctcaggccc	aggagtccag	gccccagcc	cctcctccct	caaaccaagg	780
gtacagatcc	ccagcccctc	ctccctcaga	cccaggagtc	cagaccccc	agcccctcnt	840
ccntcagacc	caggagtcca	gcccctcctc	cntcagacgc	aggagtccag	accccccagc	900
ccntcntccg	tcagaccacg	gggtgcaggc	cccccaaccc	tcntccntca	gagtcagagg	960
tccaagcccc	caaccctctg	ttccccagac	ccagaggtnc	aggtcccagc	ccctcctccc	1020
tcagaccacg	cgttccaatg	ccacctagan	tntccctgta	cacagtgcc	ccttgtggca	1080
ngttgaccca	accttaccag	ttggtttttc	attttttgtc	cctttccct	agatccagaa	1140
ataaagtnta	agagaagcgc	aaaaaaa				1167

&lt;210&gt; 176

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT



&lt;222&gt; (1)...(205)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 176

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1      5      10      15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
      20      25      30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
      35      40      45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
      50      55      60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
      65      70      75      80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
      85      90      95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
      100      105      110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
      115      120      125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
      130      135      140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
      145      150      155      160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
      165      170      175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
      180      185      190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
      195      200      205

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&lt;210&gt; 177

&lt;211&gt; 1119

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 177

```

gcgcactcgc agccctggca ggcggcactg gtcattgaaa acgaattggt ctgctcgggc      60
gtcctgggtgc atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctctacacc      120
atcgggctgg gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag      180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg      240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct      300
tcgcagtgcc ctaccgcggg gaactcttgc ctctgttctg gctggggtct gctggcgaac      360
gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagcttcc      420
caaccctggc agggttgtac catttcggca acttccagt caaggacgtc ctgctgcatc      480
ctcactgggt gctcactact gctcactgca tcacccgaa cactgtgatc aactagccag      540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt      600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc      660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc      720
tgacctacag aggtgaggga tcatatagct cttcaaggat gctggtactc ccctcacaaa      780
ttcattttctc ctgtgttagt gaaagggtgc ccctctggag cctcccaggg tgggtgtgca      840
ggtcacaatg atgaatgtat gatcgtgttc ccattacca aagccttta atccctcatg      900
ctcagtcacac cagggcaggc cttagcattt ttcatctagt gtatgctgtc cattcatgca      960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg      1020
gaggtgaggg agagggccca tgggtcaatg ggatctgtgc agttgtaaca cattaggtgc      1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaaa      1119

```

&lt;210&gt; 178

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

<220>  
 <221> VARIANT  
 <222> (1)...(164)  
 <223> Xaa = Any Amino Acid

<400> 178  
 Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp  
 1 5 10 15  
 Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu  
 20 25 30  
 Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val  
 35 40 45  
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu  
 50 55 60  
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65 70 75 80  
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85 90 95  
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val  
 100 105 110  
 Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu  
 115 120 125  
 Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg  
 130 135 140  
 Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser  
 145 150 155 160  
 Pro Gly Thr Leu

<210> 179  
 <211> 250  
 <212> DNA  
 <213> Homo sapien

<400> 179  
 ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60  
 ccagctgccc ccggccgggg gatgcgaggc tcggagcacc cttgcccggc tgtgattgct 120  
 gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgctga 180  
 aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa 240  
 aaaaaaaaaa 250

<210> 180  
 <211> 202  
 <212> DNA  
 <213> Homo sapien

<400> 180  
 actagtccag tgtggtggaa ttccattgtg ttggggcccaa cacaatggct acctttaaca 60  
 tcacccagac ccgcccctg ccgctgccc acgctgctgc taacgacagt atgatgctta 120  
 ctctgtact cggaaactat ttttatgtaa ttaatgtatg ctttctgtgt tataaatgcc 180  
 tgatttaaaa aaaaaaaaaa aa 202

<210> 181  
 <211> 558  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(558)  
 <223> n = A,T,C or G

60

```

<400> 181
tccytttkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg      60
aatgtttagg cagtgttagt aatttcytcg taatgattct gttattactt tcctnattct      120
ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa      180
ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca      240
aaattatgca agttagtaat tactcagggt taactaaatt actttaatat gctgttgaac      300
ctactctgtt ccttggctag aaaaaattat aaacaggact ttgttagttt gggaagccaa      360
attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw      420
ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt      480
aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gactttattc      540
caaaaaaaaa aaaaaaaaaa

```

```

<210> 182
<211> 479
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(479)
<223> n = A,T,C or G

```

```

<400> 182
acagggwttk grggatgcta agsccccrga rwtggtttga tccaaccctg gcttwttttc      60
agaggggaaa atggggccta gaagttacag mscatytagy tgggtgcgmg gcacccctgg      120
cstcacacag astcccgagt agctgggact acaggcacac agtcaactga gcaggccctg      180
ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca      240
ctaaggtaaa actttccac ccagaaaagg caacttagat aaaatcttag agtactttca      300
tactmttcta agtcctcttc cagcctcact kkgagtcctm cytggggggt gataggaant      360
ntctcttggc tttctcaata aartctctat ycatctcatg ttttaatttg tacgcatara      420
awtgstgara aaattaaaat gttctggtty mactttaaaa araaaaaaaa aaaaaaaaaa      479

```

```

<210> 183
<211> 384
<212> DNA
<213> Homo sapien

```

```

<400> 183
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactgggtgcc      60
agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtgggtg cttcagtgtc      120
ggtgccagcc tgaccgccac tctcacattt gggtctctcg ctggccttgg tggagctggt      180
gccagcacca gtggcagctc tgggtgcctgt ggtttctcct acaagtgaga ttttagatat      240
tgttaatcct gccagtcttt ctcttcaagc cagggtgcat cctcagaaac ctactcaaca      300
cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt      360
gccatttcaa aaaaaaaaaa aaaa

```

```

<210> 184
<211> 496
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(496)
<223> n = A,T,C or G

```

```

<400> 184
accgaattgg gaccgctggc ttataagcga tcatgtyynt ccrgtatcac ctcaacgagc      60
agggagatcg agtctatacg ctgaagaaat ttgaccgatg gggacaacag acctgtctag      120
cccatcctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga      180
aacgcttcaa ggtgctcatg acccagcaac cggcacctgt cctctgaggg tcccttaaac      240
tgatgtcttt tctgccacct gttacccttc ggagactccg taaccaaaact cttcgactg      300

```

tgagccctga	tgcctttttg	ccagccatac	tctttggcat	ccagtctctc	gtggcgattg	360
attatgcttg	tgtgaggcaa	tcatggtggc	atcacccata	aagggaacac	atttgacttt	420
tttttctcat	attttaaatt	actacmagaw	tattwmagaw	waaatgawtt	gaaaaactst	480
taaaaaaaaa	aaaaaa					496

&lt;210&gt; 185

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 185

gctggtagcc	tatggcgkgg	cccacggagg	ggctcctgag	gccacggrac	agtgacttcc	60
caagtatcyt	gcgcsgegtc	ttctaccgtc	cctacctgca	gatcttcggg	cagattcccc	120
aggaggacat	ggacgtggcc	ctcatggagc	acagcaactg	yticgtcggag	cccggcttct	180
gggcacaccc	tcctggggcc	caggcgggca	cctgcgtctc	ccagtatgcc	aactggctgg	240
tggtgctgct	cctcgtcatc	ttcctgctcg	tggccaacat	cctgctggtc	aacttgctca	300
ttgccatgtt	cagttacaca	ttcggcaaa	tacagggcaa	cagcgatctc	tactgggaag	360
gcgcagcgtt	accgcctcat	ccgg				384

&lt;210&gt; 186

&lt;211&gt; 577

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(577)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 186

gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cytctcggca	tcttggggcg	gcntaatatt	120
ccaggaaact	ctcaatcaag	tcaccgtcga	tgaaacctgt	gggctgggtc	tgtcttcgcg	180
tcgggttgaa	aggatctccc	agaaggagtg	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcca	ttctgcatgt	ccagcaggag	gttgatccag	ctctctgaca	gtgaggtcac	300
cagccctatc	atgccgttga	mcgtgccgaa	garcaccgag	ccttgtgtgg	gggkkgaa	360
ctcaccacaga	ttctgcatta	ccagagagcc	gtggcaaaag	acattgacaa	actcgcccag	420
gtggaaaaag	amcamctcct	ggargtgctn	gccgctcctc	gtcmgttggt	ggcagcgctw	480
tccttttgac	acacaaaaca	gttaaaggca	ttttcagccc	ccagaaantt	gtcatcatcc	540
aagatntcgc	acagcactna	tccagttggg	attaaat			577

&lt;210&gt; 187

&lt;211&gt; 534

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(534)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 187

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgstg	agaatycatw	60
actkggaaaa	gmaacattaa	agcctggaca	ctggtattaa	aattcacaat	atgcaacact	120
ttaaacagtg	tgtcaatctg	ctcccyynac	tttgtcatca	ccagtctggg	aakaagggtg	180
tgccttattc	acacctgtta	aaagggcgct	aagcattttt	gattcaacat	cttttttttt	240
gacacaagtc	cgaaaaaagc	aaaagttaac	agttatyaat	ttgttagcna	attcactttc	300
ttcatggggac	agagccatyt	gatttaaaaa	gcaaattgca	taatattgag	cttyggggagc	360
tgatatttga	gcggaagagt	agcctttcta	cttcaccaga	cacaactccc	tttcatattg	420
ggatgttnac	naaagtwtatg	tctctwacag	atgggatgct	tttgtggcaa	ttctgttctg	480
aggatctccc	agtttattta	ccacttgcac	aagaaggcgt	tttcttcctc	aggc	534

<210> 188  
 <211> 761  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(761)  
 <223> n = A,T,C or G

<400> 188  
 agaaaccagt atctctnaaa acaacctctc ataccttggt gacctaatgt tgtgtgcgtg 60  
 tgtgtgtgcg cgcatattat atagacaggc acatcttttt tacttttgta aaagcttatg 120  
 cctcttttgt atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct 180  
 ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt 240  
 tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc ctkgackarg 300  
 ggggacaaag aaaagcaaaa ctgamcataa raaacaatwa cctgggtgaga arttgcataa 360  
 acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtktt wtctccctt 420  
 gcaaaaaaca tgtacngact tcccgttgag taatgccaaag ttgttttttt tatnataaaa 480  
 cttgcccttc attacatgtt tnaaagtggg gtgggtggcc aaaatattga aatgatggaa 540  
 ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac 600  
 atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta 660  
 tttttctgtn ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac 720  
 gaaaataata acattgaaga aaananaaaa aaanaaaaaa a 761

<210> 189  
 <211> 482  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(482)  
 <223> n = A,T,C or G

<400> 189  
 tttttttttt ttgcccgatn ctactatttt attgcaggan gtgggggtgt atgcaccgca 60  
 caccgggggt atnagaagca agaaggaagg agggagggca cagccccttg ctgagcaaca 120  
 aagccgcctg ctgccttctc tgtctgtctc ctgggtgcagg cacatgggga gaccttcccc 180  
 aaggcagggg ccaccagtcg aggggtggga atacaggggg tgggangtgt gcataagaag 240  
 tgataggcac aggcaccccg gtacagaccc ctccgctcct gacaggtnga ttccgaccag 300  
 gtcattgtgc cctgcccagg cacagcgtn atctggaaa gacagaatgc ttcccttttc 360  
 aaatttggt ngtcatngaa ngggcanttt tccaantng gctnggtctt ggtacnctg 420  
 gttcggccca gctcncgctc caaaaantat tcaccennct ccnaattgct tgcnggnccc 480  
 cc 482

<210> 190  
 <211> 471  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(471)  
 <223> n = A,T,C or G

<400> 190  
 tttttttttt ttttaaaaca gtttttcaca acaaaattta ttagaagaat agtgggtttg 60  
 aaaactctcg catccagtga gaactacat acaccacatt acagctngga atgtntctca 120  
 aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag 180  
 cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt 240  
 taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt 300

```

tgaaaaattt catgtatgca atccaaccaa agaacttnat tggatgatcat gantncteta 360
ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacncngt acaaaaaanaa 420
tctgtaattn anttcaacct ccgtacngaa aaatntntnt tatacactcc c 471

```

<210> 191

<211> 402

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(402)

<223> n = A,T,C or G

<400> 191

```

gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct 60
gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa 120
attcttcacc agtcacatct tctaggacct ttttggattc agttagtata agctcttcca 180
cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaagg aattyaattg 240
ctcgttctct aacaatgtcc tctccttgaa gtatttggct gaacaacca cctaaagtcc 300
ctttgtgcat ccattttaaa tatacttaat agggcattgk tncactaggt taaattctgc 360
aagagtcac tgtctgcaa agttgcgtta gtatatctgc ca 402

```

<210> 192

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(601)

<223> n = A,T,C or G

<400> 192

```

gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnnaact 60
ggtctacccc acatgggagc agcatgccgt agntatataa gggtcattccc tgagtcagac 120
atgcytyttt gaytaccgtg tgccaagtgc tgggtgattct yaacacacyt ccatcccgyt 180
cttttggga aaaactggca cttktctgga actagcarga catcacttac aaattcaccc 240
acgagacact tgaaaagggt aacaaaagcga ytcttgcat gctttttgtc cctccggcac 300
cagttgtcaa tactaaccgg ctggtttgcc tccatcacat ttgtgatctg tagctctgga 360
tacatctcct gacagtactg aagaacttct tcttttggtt caaaagcacc tcttggtgcc 420
tgttggatca ggttcccatt tcccagtcyg aatgttcaca tggcatattt wacttcccac 480
aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag 540
cctcgatgta gccggccagc gccaaaggcag gcgcctgtgag ccccaccagc agcagaagca 600
g 601

```

<210> 193

<211> 608

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(608)

<223> n = A,T,C or G

<400> 193

```

atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact 60
ggtcccgtg tagcccagc gactctccac ctgctggaag cggttgatgc tgactcytt 120
cccaacgcg gcagmagcgg gscgggtcaa tgaactccay tcgtggcttg gggtkgacgg 180
tkaagtgcag gaagaggctg accacctgc ggtccaccag gatgcccagc tgtgctggac 240
ctgcagcgaa actcctcgat ggatcatgagc gggaagcgaa tgaggcccag ggccttgccc 300

```

```

agaaccttcc gcctgttctc tggcgtcacc tgcagctgct gccgctgaca ctgggcctcg      360
gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgccagtg tgctcgctc      420
caggammgsc accagcgtgt ccaggtcaat gtcgggtgaag ccctccgcgg gtratggcgt      480
ctgcagtgtt tttgtcgatg ttctccaggc acaggctggc cagctgcggg tcatcgaaga      540
gtcgcgcctg cgtgagcagc atgaaggcgt tgctcggtcg cagttcttct tcaggaactc      600
cacgcaat                                         608

```

```

<210> 194
<211> 392
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

```

```

<400> 194
gaacggctgg accttgccctc gcattgtgct tgctggcagg gaataccttg gcaagcagyt      60
ccagtccgag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggccttcccc      120
tccgcctcaa tgcagaacca gtagtgggag cactgtgttt agagttaaga gtgaacactg      180
tttgatttta cttgggaatt tcctctgtta tatagctttt cccaatgcta atttccaaac      240
aacaacaaca aaataacatg tttgcctgtt aagtgtata aaagtagggtg attctgtatt      300
taaagaaaat attactgtta catatactgc ttgcaatttc tgtatttatt gktnctstgg      360
aaataaatat agttattaaa ggttgtcant cc                                         392

```

```

<210> 195
<211> 502
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(502)
<223> n = A,T,C or G

```

```

<400> 195
ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg      60
ccgagctgag gcagatgttc ccacagtgc cccagagcc stgggstata gtytctgacc      120
cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc      180
aagggaaggc cccattccgg ggstgttccc cgaggaggaa gggaaagggc tctgtgtgcc      240
ccccasgagg aagaggccct gagtcctggg atcagacacc ccttcacgtg tatccccaca      300
caaatgcaag ctcaccaagg tcccctctca gtccccttcc stacaccctg amcggccact      360
gscscacacc caccagagc acgccacccg ccatggggar tgtgctcaag gartcgcnng      420
gcarcgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt      480
gctnanaaaa aaaaanaaaa aa                                         502

```

```

<210> 196
<211> 665
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(665)
<223> n = A,T,C or G

```

```

<400> 196
ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc      60
cctctggaag ccttgccgag agcggacttt gtaattgttg gagaataact gctgaatttt      120
wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga      180
actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkac      240

```

```

aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt 300
attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact 360
tcacttggtt attttattgt aaatgarta caaaattcctt aatttaagar aatggtagt 420
watatttatt tcattaattt ctttcctkgt ttacgtwaat ttgaaaaga wtgcatgatt 480
tcttgacaga aatcgatctt gatgctgtgg aagtagtttg acccacatcc ctatgagttt 540
ttcttagaat gtataaagg ttagagccat cnaacttcaa agaaaaaat gaccacatac 600
tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan 660
aagtg 665

```

```

<210> 197
<211> 492
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(492)
<223> n = A,T,C or G

```

```

<400> 197
tttntttttt ttttttttgc aggaaggatt ccatttattg tggatgcatt ttcacaatat 60
atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg 120
aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtaaa gatnacagag 180
aattatagtc naaccagtaa acnaggaatt tacttttcaa aagattaaat ccaaactgaa 240
caaaattcta ccctgaaact tactccatcc aaatatgtga ataanagtca gcagtgtac 300
attctcttct gaactttaga ttttctagaa aaatatgtaa tagtgatcag gaagagctct 360
tgttcaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc 420
catttcactc ccacacggg agtcaatgct acctgggaca cttgtatttt gttcatnctg 480
ancntggctt aa 492

```

```

<210> 198
<211> 478
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(478)
<223> n = A,T,C or G

```

```

<400> 198
ttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa 60
tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac 120
tgagtatatt ttgaaaagga caagttaa aa gtanacncat attgccganc atancacatt 180
tatacatggc ttgattgata ttagcacag canaaactga gtgagttacc agaaanaaat 240
natatatgtc aatcngattt aagatacaaa acagatccta tggtagatan catcntgtag 300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta 360
agcattctag tacctctact ccatgggttaa gaatcgtaca cttatgttta catatgtnc 420
gggtaagaat tgtgttaagt naanttatgg agaggtccan gagaaaaatt tgatncaa 478

```

```

<210> 199
<211> 482
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(482)
<223> n = A,T,C or G

```

```

<400> 199
agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcaactgaca atcagacct 60

```



tgctagttcc	tgtcatctat	tcgctactaa	atgcagactg	gaggggacca	aaaaggggca	120
tcaactccag	ctggattatt	ttggagcctg	caaacttatt	cctacttgta	cggactttga	180
agtgattcag	tttctctac	ggatgagaga	ctgggtcaag	aatatcctca	tgcagcttta	240
tgaagccnac	tctgaacacg	ctggttatct	nagatgagaa	ncagagaaat	aaagtcnaga	300
aaatttacct	ggangaaaag	aggctttngg	ctggggacca	tcccattgaa	ccttctctta	360
anggacttta	agaanaaaact	accacatgtn	tgtngtatcc	tggtgccngg	ccgtttantg	420
aacntngacn	ncacccttnt	ggaatanant	cttgacngcn	tcctgaactt	gctcctctgc	480
ga						482

&lt;210&gt; 200

&lt;211&gt; 270

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(270)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 200

cggccgcaag	tgcaactcca	gctggggccg	tgccgacgaa	gattctgcca	gcagttgggtc	60
cgactgcgac	gacggcgcg	gcgacagtcg	caggtgcagc	gcgggcgcct	ggggtcttgc	120
aaggctgagc	tgacgccgca	gaggtcgtgt	cacgtcccac	gaccttgacg	ccgtcgggga	180
cagccggaac	agagcccgtt	gaangcggga	ggcctcgggg	agcccctcgg	gaagggcggc	240
ccgagagata	cgcaggtgca	ggtggccgcc				270

&lt;210&gt; 201

&lt;211&gt; 419

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(419)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 201

tttttttttt	ttttggaatc	tactgcgagc	acagcaggtc	agcaacaagt	ttattttgca	60
gctagcaagg	taacagggta	gggcatggtt	acatgttcag	gtcaacttcc	tttgtcgtgg	120
ttgattgggt	tgtctttatg	ggggcggggt	ggggtagggg	aaancgaagc	anaantaaca	180
tggagtgggt	gcacctccc	tgtagaacct	ggttacnaaa	gcttggggca	gttcacctgg	240
tctgtgaccg	tcattttctt	gacatcaatg	ttattagaag	tcaggatatc	ttttagagag	300
tccactgtnt	ctggagggag	attagggttt	cttgccaana	tccaancaaa	atccacntga	360
aaaagttgga	tgatncangt	acngaatacc	ganggcatan	ttctcatant	cgggtggcca	419

&lt;210&gt; 202

&lt;211&gt; 509

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(509)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 202

ttnttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
tggcacttta	tccattttta	tttcaaaatg	tctacaaant	ttnaatncnc	cattatacng	120
gtnattttnc	aaaatctaaa	nnttatctaa	atntnagcca	aantccttac	ncaaattnaa	180
tacnncnaaa	aatcaaaaaa	atacntntct	ttcagcaaac	ttngttacat	aaattaaaaa	240
aatatatacg	gctgggtgtt	tcaaagtaca	attatcttaa	cactgcaaac	atnttttnaa	300
ggaactaaaa	taaaaaaaaa	cactnccgca	aaggttaaag	ggaacaacaa	attcntttta	360

```

caacancnnc nattataaaa atcatatctc aaatcttagg ggaatatata cttcacacng    420
ggatcttaac ttttactnca ctttgtttat ttttttanaa ccattgtntt gggccaaca    480
caatggnaat nccnccnncn tggactagt    509

```

&lt;210&gt; 203

&lt;211&gt; 583

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(583)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 203

```

tttttttttt ttttttttga cccccctctt ataaaaaaca agttaccatt ttatttttact    60
tacacatatt ttttttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac    120
taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaaatc tgcctaaagt    180
gaaaatcttc tctagctctt ttgactgtaa atttttgact cttgtaaaac atccaaattc    240
atttttcttg tctttaaaat tatctaattc ttccattttt tccctattcc aagtcaattt    300
gcttctctag cctcatttcc tagctcttat ctactattag taagtggctt ttttcctaaa    360
agggaaaaca ggaagagana atggcacaca aaacaaacat tttatattca tatttctacc    420
tacgttaata aaatagcatt ttgtgaagcc agctcaaaaag aaggcttaga tccttttatg    480
tccatttttag tcaactaaacg atatcnaaag tgccagaatg caaaagggtt gtgaacattt    540
attcaaaagc taatataaga tatttcacat actcatcttt ctg    583

```

&lt;210&gt; 204

&lt;211&gt; 589

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(589)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 204

```

ttttttttnt tttttttttt ttttttnctc ttcttttttt ttganaatga ggatcgagtt    60
tttctctctc tagatagggc atgaagaaaa ctcatctttc cagcttttaa ataacaatca    120
aatctcttat gctatatcat attttaagtt aaactaatga gtcactggct tatcttctcc    180
tgaaggaaat ctgttcattc ttctcattca tatagttata tcaagtacta ccttgcatat    240
tgagaggttt ttcttctcta tttacacata tatttccatg tgaatttgta tcaaaccctt    300
attttcatgc aaactagaaa ataattgtnt cttttgcata agagaagaga acaatatnag    360
cattacaaaa ctgctcaaat tgtttgttaa gnttatccat tataattagt tnggcaggag    420
ctaatacaaa tcacatttac ngacnagcaa taataaaaact gaagtaccag ttaaatatcc    480
aaaataattt aaggaacatt tttagcctgg gtataattag ctaattcact ttacaagcat    540
ttattnagaa tgaattcaca tgttattatt ccntagccca acacaatgg    589

```

&lt;210&gt; 205

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(545)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 205

```

ttttnttttt ttttttcagt aataatcaga acaatattta tttttatatt taaaattcat    60
agaaaagtgc cttacattta ataaaagttt gtttctcaa gtgatcagag gaattagata    120
tngtcttgaa caccaatatt aatttgagga aaatacacca aaatacatta agtaaattat    180

```

```

ttaagatcat agagcttgta agtgaaaaga taaaatttga cctcagaaac tctgagcatt 240
aaaaatccac tattagcaaa taaattacta tggacttctt gctttaattt tgtgatgaat 300
atggggtgtc actggtaaac caacacattc tgaaggatac attacttagt gatagattct 360
tatgtacttt gctanatnac gtggatatga gttgacaagt ttctctttct tcaatctttt 420
aaggggcnga ngaaatgagg aagaaaagaa aaggattacg catactgttc tttctatngg 480
aaggattaga tatgtttcct ttgccaatat taaaaaata ataatgttta ctactagtga 540
aacc 545

```

<210> 206

<211> 487

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(487)

<223> n = A,T,C or G

<400> 206

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tttttttttt ttttttagtc aagtttctna tttttattat aattaaagtc ttggtcattt 60
catttatttag ctctgcaact tacatattta aattaaagaa acgttnttag acaactgtna 120
caatttataa atgtaagggtg ccattattga gtanatatat tcctccaaga gtggatgtgt 180
cccttctccc accaactaat gaancagcaa cattagttaa attttattag tagatnatac 240
actgctgcaa acgctaattc tcttctccat ccccatgtng atattgtgta tatgtgtgag 300
ttggnagaa tgcatanca atctnacaat caacagcaag atgaagctag gcntgggctt 360
tcggtgaaaa tagactgtgt ctgtctgaat caaatgatct gacctatcct cgggtggcaag 420
aactcttcga accgcttcct caaaggcngc tgccacattt gtggcntctn ttgcacttgt 480
ttcaaaa 487

```

<210> 207

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 207

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tgaattggct aaaagactgc atttttanaa ctagcaactc ttatttcttt cctttaaaaa 60
tacatagcat taaatcccaa atcctattta aagacctgac agcttgagaa ggctactact 120
gcatttatag gaccttctgg tggttctgct gttacntttg aantctgaca atccttgana 180
atctttgcat gcagaggagg taaaagggtat tggattttca cagaggaana acacagcgca 240
gaaatgaagg ggccaggctt actgagcttg tccactggag ggctcatggg tgggacatgg 300
aaaagaaggc agcctaggcc ctggggagcc ca 332

```

<210> 208

<211> 524

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(524)

<223> n = A,T,C or G

<400> 208

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agggcggtggt gcggaggggc ttactgtttt gtctcagtaa caataaatac aaaaagactg 60
gttgtgttcc ggccccatcc aaccacgaag ttgatttctc ttgtgtgcag agtgactgat 120
tttaaaggac atggagcttg tcacaatgtc acaatgtcac agtgtgaagg gcacactcac 180
tcccgcgtga ttcacattta gcaaccaaca atagctcatg agtccatact tgtaaatact 240

```

tttggcagaa	tacttnttga	aacttgcaga	tgataactaa	gatccaagat	atttcccaaa	300
gtaaatagaa	gtgggtcata	atattaatta	cctgttcaca	tcagcttcca	tttacaagtc	360
atgagccag	acactgacat	caaactaagc	ccacttagac	tcctcaccac	cagtctgtcc	420
tgtcatcaga	caggaggctg	tcaccttgac	caaattctca	ccagtcaatc	atctatccaa	480
aaaccattac	ctgatccact	tccggtaatg	caccaccttg	gtga		524

&lt;210&gt; 209

&lt;211&gt; 159

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 209

gggtgaggaa	atccagagtt	gccatggaga	aaattccagt	gtcagcattc	ttgctccttg	60
tggccctctc	ctacactctg	gccagagata	ccacagtcaa	acctggagcc	aaaaaggaca	120
caaaggactc	tcgacccaaa	ctgcccacga	ccctctcca			159

&lt;210&gt; 210

&lt;211&gt; 256

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(256)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 210

actccctggc	agacaaaggc	agaggagaga	gctctgttag	ttctgtgttg	ttgaactgcc	60
actgaatttc	tttccacttg	gactattaca	tgccanttga	gggactaatg	gaaaaacgta	120
tggggagatt	ttanccaatt	tangtntgta	aatggggaga	ctggggcagg	cgggagagat	180
ttgcagggtg	naaatgggan	ggctggtttg	ttanatgaac	agggacatag	gaggtaggca	240
ccaggatgct	aatca					256

&lt;210&gt; 211

&lt;211&gt; 264

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(264)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 211

acattgtttt	tttgagataa	agcattgaga	gagctctcct	taacgtgaca	caatggaagg	60
actggaacac	ataccacacat	ctttgttctg	agggataatt	ttctgataaa	gtcttgctgt	120
atattcaagc	acatatgtta	tatattattc	agttccatgt	ttatagccta	gttaaggaga	180
ggggagatac	attcngaaaag	aggactgaaa	gaaatactca	agtnngaaaa	cagaaaaaga	240
aaaaaaggag	caaatgagaa	gcct				264

&lt;210&gt; 212

&lt;211&gt; 328

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(328)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 212

acccaaaaat	ccaatgctga	atatttggtc	tcattattcc	canattcttt	gattgtcaaa	60
------------	------------	------------	------------	------------	------------	----

ggatttaatg	ttgtctcagc	ttgggcactt	cagttaggac	ctaaggatgc	cagccggcag	120
gtttatatat	gcagcaacaa	tattcaagcg	cgacaacagg	ttattgaact	tgcccgccag	180
ttnaatttca	ttcccattga	cttgggatcc	ttatcatcag	ccagagagat	tgaaaattta	240
cccctacnac	tctttactct	ctgganaggg	ccagtgggtg	tagctataag	cttggccaca	300
tttttttttc	ctttattcct	ttgtcaga				328

&lt;210&gt; 213

&lt;211&gt; 250

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(250)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 213

acttatgagc	agagcgacat	atccnagtgt	agactgaata	aaactgaatt	ctctccagtt	60
taaagcattg	ctcactgaag	ggatagaagt	gactgccagg	agggaaagta	agccaaggct	120
cattatgccca	aagganatat	acatttcaat	tctccaaact	tcttcctcat	tccaagagtt	180
ttcaatattt	gcatgaacct	gctgataanc	catgttaana	aacaaatata	tctctnacct	240
tctcatcggt						250

&lt;210&gt; 214

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(444)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 214

accagaatc	caatgctgaa	tatttggtct	cattattccc	agattctttg	attgtcaaag	60
gatttaattg	tgtctcagct	tgggcacttc	agttaggacc	taaggatgcc	agccggcagg	120
tttatatatg	cagcaacaat	attcaagcgc	gacaacagg	tattgaactt	gcccggcagg	180
tgaatttcat	tcccattgac	ttgggatcct	tatcatcagc	canagagatt	gaaaatttac	240
ccctacgact	ctttactctc	tggagagggc	cagtgggtgt	agctataagc	ttggccacat	300
ttttttttcc	tttattcctt	tgtcagagat	gcgattcatc	catatgctan	aaaccaacag	360
agtgactttt	acaaaattcc	tataganatt	gtgaataaaa	ccttacctat	agttgccatt	420
actttgctct	ccctaataata	cctc				444

&lt;210&gt; 215

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(366)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 215

acttatgagc	agagcgacat	atccaagtgt	anactgaata	aaactgaatt	ctctccagtt	60
taaagcattg	ctcactgaag	ggatagaagt	gactgccagg	agggaaagta	agccaaggct	120
cattatgccca	aagganatat	acatttcaat	tctccaaact	tcttcctcat	tccaagagtt	180
ttcaatattt	gcatgaacct	gctgataagc	catgttgaga	aacaaatata	tctctgacct	240
tctcatcggt	aagcagaggg	tgtaggcaac	atggaccata	gcgaanaaaa	aacttagtaa	300
tccaagctgt	tttctacact	gtaaccagg	ttccaaccaa	ggtggaaatc	tcctatactt	360
ggtgcc						366

<210> 216  
 <211> 260  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(260)  
 <223> n = A,T,C or G

<400> 216  
 ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgct 60  
 caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctntnc atttttttat 120  
 taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttnggctgga aaatttaaaa 180  
 atcaaaaatt tctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240  
 aattcttctt tccctcctt 260

<210> 217  
 <211> 262  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(262)  
 <223> n = A,T,C or G

<400> 217  
 acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60  
 tcttgctat aattttctat ttttaataagg aaatagcaaa ttgggggtgg gggaatgtag 120  
 ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180  
 atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240  
 atatccttca tgcttgtaaa gt 262

<210> 218  
 <211> 205  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(205)  
 <223> n = A,T,C or G

<400> 218  
 accaaggtgg tgcattaccg gaantggatc aangacacca tctgtggcaa cccctgagca 60  
 cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccagactc 120  
 aggctcccc agttctactg acctttgtcc ttangntna ngtccagggt tgctaggaaa 180  
 anaaatcagc agacacaggt gtaaa 205

<210> 219  
 <211> 114  
 <212> DNA  
 <213> Homo sapien

<400> 219  
 tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gccccatcca 60  
 accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220  
 <211> 93  
 <212> DNA

<213> Homo sapien

<400> 220

actagccagc acaaaaaggca gggtagcctg aattgcttcc tgctctttac atttctttta 60  
aaataagcat ttagtgctca gtcctactg agt 93

<210> 221

<211> 167

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(167)

<223> n = A,T,C or G

<400> 221

actangtgca ggtgcgcaca aatatttgct gatattccct tcatcttgga ttccatgagg 60  
tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc 120  
ccccactac cttccctgac gtcccccana aatcacccaa cctctgt 167

<210> 222

<211> 351

<212> DNA

<213> Homo sapien

<400> 222

agggcggtggt gcggaggggcg gtactgacct cattagtagg aggatgcatt ctggcacccc 60  
gttcttcacc tgtcccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa 120  
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa 180  
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt 240  
taggtgagca tgattagaga gcttgtagggt tgcttttaca tatatctggc atatttgagt 300  
ctcgatcaaa aacaatagat tggtaaagggt ggtattattg tattgataag t 351

<210> 223

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 223

aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat 60  
tggttaattat ggtcaattta atwrtrttkt ggggcatttc cttacattgt cttgacaaga 120  
ttaaaatgtc tgtgccaataa ttttgatttt tatttggaga cttcttatca aaagtaatgc 180  
tgccaaagga agtctaagga attagtagtg ttcccmccac ttgtttggag tgtgctattc 240  
taaaagattt tgatttcctg gaatgacaat tatattttta ctttgggtgg ggaaanagtt 300  
ataggaccac agtcttcact tctgatactt gtaaattaat cttttattgc acttgttttg 360  
accattaagc tatatgttta aaa 383

<210> 224

<211> 320

<212> DNA

<213> Homo sapien

<400> 224

cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga 60  
aaaagtttgt gacattgtag tagggagtgt gtacccttta ctcccatca aaaaaaaat 120  
ggatacatgg ttaaaggata raagggaat attttatcat atgttctaaa agagaaggaa 180

gagaaaaatac	tacttttctcr	aaatggaagc	ccttaaaggt	gctttgatac	tgaaggacac	240
aaatgtggcc	gtccatcctc	ctttaragtt	gcatgacttg	gacacggtaa	ctgttgacgt	300
tttaractcm	gcattgtgac					320

<210> 225  
 <211> 1214  
 <212> DNA  
 <213> Homo sapien

<400> 225						
gaggactgca	gcccgcactc	gcagccctgg	caggcggcac	tggtcatgga	aaacgaattg	60
ttctgctcgg	gcgtcctggt	gcacccgcag	tgggtgctgt	cagccgcaca	ctgtttccag	120
aaactcctaca	ccatcgggct	gggcctgcac	agtcttgagg	ccgaccaaga	gccagggagc	180
cagatgggtg	aggccagcct	ctccgtacgg	cacccagagt	acaacagacc	cttgctcgct	240
aacgacctca	tgctcatcaa	gttgacgaa	tccgtgtccg	agtctgacac	catccggagc	300
atcagcattg	cttcgcagtg	ccctaccgcg	gggaactctt	gcctcgtttc	tggtctgggt	360
ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	tgaacgtgtc	ggtggtgtct	420
gaggaggtct	gcagtaagct	ctatgaccgg	ctgtaccacc	ccagcatggt	ctgcgccggc	480
ggagggcaag	accagaagga	ctcctgcaac	ggtgactctg	ggggggccct	gatctgcaac	540
gggtacttgc	agggccttgt	gtctttcgga	aaagccccgt	gtggccaagt	tggtctgcca	600
ggtgtctaca	ccaacctctg	caaattcact	gagtggatag	agaaaaccgt	ccaggccagt	660
taactctggg	gactgggaac	ccatgaaatt	gacccccaaa	tacatcctgc	ggaaggaatt	720
caggaatata	tggtcccagc	ccctcctccc	tcaggcccag	gagtcaggc	ccccagcccc	780
tcctccctca	aaccaagggt	acagatcccc	agcccctcct	ccctcagacc	caggagtcca	840
gacccccag	cccctcctcc	ctcagaccga	ggagtccagc	ccctcctccc	tcagaccag	900
gagtcagac	ccccagcccc	ctcctccctc	agaccagggg	gtccaggccc	ccaacccctc	960
ctccctcaga	ctcagaggtc	caagccccca	acccctcctt	ccccagaccc	agaggtccag	1020
gtcccagccc	ctcctccctc	agaccagcgg	gtccaatgcc	acctagactc	tcctgtaca	1080
cagtgcctcc	ttgtggcacg	ttgaccacac	cttaccagtt	ggtttttcat	ttttgtccc	1140
tttcccttag	atccagaaat	aaagtctaag	agaagcgcaa	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa	aaaa					1214

<210> 226  
 <211> 119  
 <212> DNA  
 <213> Homo sapien

<400> 226						
acccagtatg	tgcagggaga	cggaacccca	tgtgacagcc	cactccacca	gggttcccaa	60
agaacctggc	ccagtcataa	tcattcatcc	tgacagtggc	aataatcacg	ataaccagt	119

<210> 227  
 <211> 818  
 <212> DNA  
 <213> Homo sapien

<400> 227						
acaattcata	gggacgacca	atgaggacag	ggaatgaacc	cggctctccc	ccagccctga	60
tttttgctac	atatgggggtc	ccttttcatt	ctttgcaaaa	acactgggtt	ttctgagaac	120
acggacgggt	cttagcacia	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttcctc	ctctggagga	aaggtggtga	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca	cgctcggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgtcccc	ttccaatcag	ccacttctga	gaacccccat	ctaacttctc	actgaaaaag	360
agggcctcct	caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaagggtg	caccctcagc	agagaagccg	agagcttaac	tctggtcgtt	tccagagaca	480
acctgctggc	tgtcttgagg	tgcgccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggacatgaag	ctgaggacac	tgggcttcaa	cactgagttg	tcattgagag	600
gacaggctct	gccctcaagc	cggctgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggtc	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtcgtgt			818



<210> 228  
 <211> 744  
 <212> DNA  
 <213> Homo sapien

<400> 228  
 actggagaca ctgttgaact tgatcaagac ccagaccacc ccagggtctcc ttcgtgggat 60  
 gtcacgacgt ttgacataacc tttggaacga gcctcctcct tggagatgg aagaccgtgt 120  
 tcgtggccga cctggcctct cctggcctgt ttcttaagat gcggagtcac atttcaatgg 180  
 taggaaaagt ggcttcgtaa aatagaagag cagtcactgt ggaactacca aatggcgaga 240  
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 ttcttttcgt taatgttcct ctgtgttgct agctgtcttc atttctggg ctaagcagca 660  
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 <212> DNA  
 <213> Homo sapien

<400> 229  
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 tgcagggttg ttgtttttta attattattg ttagaaacgt caccacagt ccctgttaat 180  
 ttgtatgtga cagccaactc tgagaaggtc ctatttttcc acctgcagag gatccagtct 240  
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 <212> DNA  
 <213> Homo sapien

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 caatataaag tcctggttca cactcaggaa cgagagctga ccaggttaag ggagaagttg 180  
 cggaaggga gagatgcctc cctctcattg aatgagcatc tccaggccct cctcactccg 240  
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 g 301

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 <211> 301  
 <212> DNA  
 <213> Homo sapien

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 ggcaacacgg gactttctcat caggaagtgg gatgtatg agctgatcaa gacggccagg 180  
 tctgaggatg gcaggatcaa tgatgtcagg ccggttggtta ccgccaatga tgaacacatt 240  
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 c 301

<210> 232  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

## &lt;400&gt; 232

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cgtgctgtac	caagtgtctg	tgccagcctg	ttacctgttc	tcactgaaaa	tctggctaata	240
gctcttgtgt	atcacttctg	attctgacaa	tcaatcaatc	aatggcctag	agcactgact	300
g						301

&lt;210&gt; 233

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 233

atgactgact	tcccagtaag	gctctctaag	gggtaagtag	gaggatccac	aggatttgag	60
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cctagaagtt	acagagcatc	tagctgggtc	gctggcaccc	ctggcctcac	acagactccc	180
gagtagctgg	gactacaggc	acacagtcac	tgaagcaggc	cctgttagca	attctatgcg	240
tacaaattaa	catgagatga	gtagagactt	tattgagaaa	gcaagagaaa	atcctatcaa	300
c						301

&lt;210&gt; 234

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 234

aggctctaca	catcgagact	catccatgat	tgatatgaat	ttaaaaatta	caagcaaaga	60
cattttattc	atcatgatgc	tttcttttgt	ttcttctttt	cgttttcttc	tttttctttt	120
tcaatttcag	caacatactt	ctcaatttct	tcaggattta	aaatcttgag	ggattgatct	180
cgcctcatga	cagcaagttc	aatgtttttg	ccacctgact	gaaccacttc	caggagtgcc	240
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t						301

&lt;210&gt; 235

&lt;211&gt; 283

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 235

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tgctttcact	aatgtctctg	aacttctgtc	cctctttgtt	catggatagt	ccaataaata	180
atgttatctt	tgaactgatg	ctcataggag	agaatataag	aactctgagt	gatatcaaca	240
ttagggattc	aaagaaatat	tagatttaag	ctcacactgg	tca		283

&lt;210&gt; 236

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 236

aggctctcca	ccaactgcct	gaagcacggg	taaaattggg	aagaagtata	gtgcagcata	60
aatactttta	aatcgatcag	atttccttaa	cccacatgca	atcttcttca	ccagaagagg	120
tcggagcagc	atcattaata	ccaagcagaa	tgcgtaatag	ataaatacaa	tggtatatag	180
tgggtagacg	gcttcatgag	tacagtgtac	tgtggtatcg	taatctggac	ttgggttgta	240
aagcatcgtg	taccagtcag	aaagcatcaa	tactcgacat	gaacgaatat	aaagaacacc	300
a						301

&lt;210&gt; 237

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 237

cagtggtagt ggtgggtggac gtggcggttg tctgtggtgcc ttttttggtg cccgtcacaa	60
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ccttggtctaa tgcctcatag taggagtcct cagaccagcc atggggatca aacatatcct	180
ttgggtagtt ggtgccaaagc tctgcaatgg cacagaatgg atcagcttct cgtaaatacta	240
gggttccgaa attctttctt cctttggata atgtagtcca tatccattcc ctccctttatc	300
t	301

&lt;210&gt; 238

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 238

gggcagggttt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt	60
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ccttgagact tccggagtcg aggcctctcca gggttcccca gcccatcaat cattttctgc	180
acccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca	240
gtgtgggacc cagggtctgt tcttcacagt aggaggtgga agggatgact aatttcttta	300
t	301

&lt;210&gt; 239

&lt;211&gt; 239

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 239

ataagcagct aggggaattct ttatttagta atgtcctaac ataaaagtgc acataactgc	60
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cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac	180
attcagccag tgagtagagt gtgaatgcc gcatcacacg tatacaggtc cttcaggga	239

&lt;210&gt; 240

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 240

ggtcctaata aagcagcagc ttccacattt taacgcaggt ttacgggtgat actgtccttt	60
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gctgggtgag ccagatgact tctgttcctt ggtcactttc ttcaatgggg cgaatggggg	180
ctgccagggt tttaaaatca tgcttcatct tgaagcacac ggtcacttca ccctcctcac	240
gctgtgggtg tactttgatg aaaataccca ctttgttggc ctttctgaag ctataatgtc	300

&lt;210&gt; 241

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 241

gaggctggt gctgaggtct ctgggctagg aagaggagtt ctgtggagct ggaagccaga	60
cctcttttga ggaaactcca gcagctatgt tgggtgtctct gagggaatgc aacaaggctg	120
ctcctccatg tattggaaaa ctgcaaaactg gactcaactg gaaggaagtg ctgctgccag	180
tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct	240
tcctcctcct gtcatacggg ctctctcaag catcctttgt tgtcaggggc ctaaaaggga	300
g	301

&lt;210&gt; 242

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien.

&lt;400&gt; 242

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tgtggcattt cctcattttc tacattgtag aatcaagagt gtaaataaat gtatatcgat	120
gtcttcaaga atatcatt cctttttcac tagaaccat tcaaaatata agtcaagaat	180
cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta	240
taagtaccca aagttttata aatcaaaagc cctaatagata accattttta gaattcaatc	300
a	301

&lt;210&gt; 243

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 243

aggtaagtcc cagtttgaag ctcaaaagat ctggtatgag cataggctca tcgacgacat	60
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tgacgtgcag tcggactctg tggccaagg gtatggctct ctcgcatga tgaccagcgt	180
gctggtttgt ccagatggca agacagtaga agcagaggct gccacggga ctgtaaccg	240
tcactaccgc atgttccaga aaggacagga gacgtccacc aatcccattg cttccatttt	300
t	301

&lt;210&gt; 244

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 244

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gtcatgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc	120
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actgtttgtc ttttgtgtat cttttttaaa ctgtaaagtt caattgtgaa aatgaatatc	300

&lt;210&gt; 245

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 245

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tatatactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt	120
aaggccagga gatattgtca ttaatgtara cttcaggaca ctagagtata gcagccctat	180
gttttcaaag agcagagatg caattaaata ttgttttagca tcaaaaaggc cactcaatac	240
agctaataaa atgaaagacc taatttctaa agcaattctt tataatttac aaagttttaa	300
g	301

&lt;210&gt; 246

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 246

ggtctgtcct acaatgcctg cttcttgaaa gaagtcggca ctttctagaa tagctaaata	60
acctgggctt attttaaaga actatttgta gctcagattg gttttcctat ggctaaaata	120
agtgtctctt gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac	180
taacaatcat actaaatata ttttgaagta caaagtttga catgctctaa agtgacaacc	240
caaatgtgtc ttacaaaaca cgttcctaac aaggtatgct ttacactacc aatgcagaaa	300
c	301

&lt;210&gt; 247

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 247

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gtgtcctgtg	ttcaggtgcg	acacacaatc	ctcatgggaa	caggatcacc	catgcgctgc	180
ccttgatgat	caaggttggg	gcttaagtgg	attaagggag	gcaagttctg	ggttccttgc	240
cttttcaaac	catgaagtca	ggctctgtat	ccctcctttt	cctaactgat	attctaacta	300
a						301

&lt;210&gt; 248

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 248

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ctaattgagac	tggttttttg	ttttttatgt	tgtgtgtcgc	agagctaaaa	actcagttcc	300
c						301

&lt;210&gt; 249

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 249

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catcgtaatg	aattattttg	aaaattaatt	ccaccatcct	ttcagattct	ggatggaaag	240
actgaatctt	tgactcagaa	ttgtttgctg	aaaagaatga	tgtgactttc	ttagtcattt	300
a						301

&lt;210&gt; 250

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 250

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ctaaaagact	actatgtgga	ataatacata	ctaataaggt	attacatgat	ttaaagacta	240
caataaaacc	aaacatgctt	ataacattaa	gaaaaacaat	aaagatacat	gattgaaacc	300
a						301

&lt;210&gt; 251

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 251

gccgaggtcc	tacatttggc	ccagtttccc	cctgcaccc	ctccagggcc	cctgcctcat	60
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c 301

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<212> DNA  
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tcatttcctt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa 180  
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag tacccaaagt 240  
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a 301

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<212> DNA  
<213> Homo sapien

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tggtctgatt gttttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg 180  
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt 240  
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g 301

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<211> 301  
<212> DNA  
<213> Homo sapien

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t 301

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<211> 302  
<212> DNA  
<213> Homo sapien

<400> 255  
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attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat 120  
tggtgatttt ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg 180  
aggaaaaagg actggaggtg gaatctttat aaaaaacaag agtgattgag gcagattgta 240  
aacattatta aaaaacaaga acaaaacaaa aaaatagaga aaaaaaccac cccaacacac 300  
aa 302

<210> 256  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 256

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aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc    120
acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcctctctat    180
aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt    240
gtggcctctc ggcctgggta gcaagaacat tcagggtagg cctaagttan tcgtgttagt    300
t                                                    301
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<210> 257

<211> 301

<212> DNA

<213> Homo sapien

<400> 257

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tccccactta tttttgtctt tcactatcgc aggccttaga agaggtctac ctgcctccag    120
tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat    180
gtcacattac tcccttcagt gatttcttgt agaagtgcc atccctgaat gccaccaaga    240
tcttaattct cactcttta atcttatctc ttgactcct ctttacaccg gagaaggctc    300
c                                                    301
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<210> 258

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 258

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cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg    180
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat    240
tggatgatccc tgggagcgcc ggtggagtaa cgttgggtcca tggaaagcag cgcccacaac    300
t                                                    301
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<210> 259

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 259

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tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggcct    240
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcctccttgg ctccagggtg    300
c                                                    301
```

<210> 260

<211> 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 260

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aagggtgtctt aacttgaaaa agattaggag tctctgggtt acaagttata attgaatgaa      120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaacia caggattaac      180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttaataaac agactgattc      240
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca      300
c                                                                    301

```

&lt;210&gt; 261

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 261

```

aaatattcga gcaaatcctg taactaatgt gtctccataa aaggctttga actcagtga      60
tctgtctcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggt      120
agcaccaact attccataga attcatcagc aggaaataaa ggctcttcag aagggttcaat      180
ggtgacatcc aatttcttct gataatttag attcctcaca accttcctag ttaagtgaag      240
ggcatgatga tcatccaaag ccagtggtgc acttactcca gactttctgc aatgaagatc      300
a                                                                    301

```

&lt;210&gt; 262

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 262

```

gaggagagcc tgttacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc      60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaacc ctgagtcacc      120
cctagacttc ctaaacagga tcctctgggg ctggaacctg gcactctgca tttgtaatga      180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgcc      240
catcattacc ccacattat aatgggatag attcagagca gatactctcc agcaaagaat      300
c                                                                    301

```

&lt;210&gt; 263

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 263

```

tttagcttgt ggtaaattgac tcacaaaact gattttaaaa tcaagttaat gtgaattttg      60
aaaattacta cttaattccta attcacaata acaatggcat taaggtttga cttgagttgg      120
ttcttagtat tatattatggt aaataggctc ttaccacttg caaataactg gccacatcat      180
taatgactga cttcccagta aggtctctta aggggtaagt angaggatcc acaggatttg      240
agatgctaag gccccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg      300
g                                                                    301

```

&lt;210&gt; 264

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 264

```

aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaascc      60

```



aatgaatgac tctaaaaaca atattttacat ttaatggttt gtagacaata aaaaaacaag 120  
 gtggatagat ctagaattgt aacattttta gaaaaccata scatttgaca gatgagaaag 180  
 ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac 240  
 acccttcata taaattcact atcttggctt gaggcactcc ataaaatgta tcacgtgcat 300  
 a 301

<210> 265  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 265  
 tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcattctttgt 60  
 cttcttctga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta 120  
 catattcttg gaagtctcta atcaactttt gttccatttg tttcatttct tcaggaggga 180  
 ttttcagttt gtcaacatgt tctctaaca cacttgccca tttctgtaaa gaatccaaag 240  
 cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg 300  
 c 301

<210> 266  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 266  
 taccgtctgc ctttctctcc atccaggcca tctgcgaatc tacatgggtc ctctatttcg 60  
 acaccagatc actcttttct ctaccacag gcttgctatg agcaagagac acaacctcct 120  
 ctcttctgtg ttccagcttc ttttctgtt cttccacccc ctttaagttct attcctgggg 180  
 atagagacac caatacccat aacctctctc ctaagcctcc ttataacca ggggtgcacag 240  
 cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgcctg 300  
 a 301

<210> 267  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 267  
 aaagagcaca ggccagctca gcctgccctg gccatctaga ctcagcctgg ctccatgggg 60  
 gttctcagtg ctgagtcacat ccaggaaaag ctcacctaga ctttctgagg ctgaatcttc 120  
 atcctcacag gcagcttctg agagcctgat attcctagcc ttgatgggtc ggagtaaacg 180  
 ctcatctga ttctctctct tctttcttt caagttggct ttcctcacat cctctgttc 240  
 aattcgcttc agcttgtctg ctttagccct catttccaga agcttcttct ctttggcatc 300  
 t 301

<210> 268  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 268  
 aatgtctcac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta 60  
 gatcttggga gagctgggtc ttctaaggag aaggaggaag gacagatgta actttggatc 120  
 tcgaagagga agtctaattg aagtaattag tcaacgggtc ttgttttagac tcttgaata 180  
 tgctgggtgg ctcagtgagc cttttgggag aaagcaagta ttattcttaa ggagtaacca 240  
 cttccattg ttctactttc taccatcate aattgtatat tatgtattct ttggagaact 300  
 a 301

<210> 269  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 269

taacaatata	cactagctat	ctttttaact	gtccatcatt	agcaccaatg	aagattcaat	60
aaaattacct	ttattcacac	atctcaaaac	aattctgcaa	attcttagtg	aagtttaact	120
atagtcacag	accttaaata	ttcacattgt	tttctatgtc	tactgaaaat	aagttcacta	180
cttttctgga	tattctttac	aaaatcttat	taaaattcct	ggtattatca	ccccaatta	240
tacagtagca	caaccacctt	atgtagtttt	tacatgatag	ctctgtagaa	gtttcacatc	300
t						301

&lt;210&gt; 270

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 270

cattgaagag	cttttgcgaa	acatcagaac	acaagtgcct	ataaaattaa	ttaagcctta	60
cacaagaata	catattcctt	ttatttctaa	ggagttaaac	atagatgtag	ctgatgtgga	120
gagcttgctg	gtgcagtgc	tattggataa	cactattcat	ggccgaattg	atcaagtcaa	180
ccaactcctt	gaactggatc	atcagaagaa	gggtggtgca	cgatatactg	cactagataa	240
tggaccaacc	aactaaattc	tctcaccagg	ctgtatcagt	aaactggctt	aacagaaaac	300
a						301

&lt;210&gt; 271

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 271

aaaaggttct	cataagatta	acaatttaaa	taaatatttg	atagaacatt	ctttctcatt	60
tttatagctc	atctttaggg	ttgatattca	gttcatgctt	cccttgctgt	tcttgatcca	120
gaattgcaat	cacttcatca	gcctgtattc	gctccaattc	tctataaagt	gggtccaagg	180
tgaaccacag	agccacagca	cacctctttc	ccttggtgac	tgccttcacc	ccatganggt	240
tcttctctcc	agatganaac	tgatcatgcg	cccacatttt	gggttttata	gaagcagtc	300
c						301

&lt;210&gt; 272

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 272

taaattgcta	agccacagat	aacaccaatc	aaatggaaca	aatcactgtc	ttcaaagtgc	60
ttatcagaaa	accaaagtga	cctggaatct	tcataatacc	taaacatgcc	gtatttagga	120
tccaataatt	ccctcatgat	gagcaagaaa	aattctttgc	gcacccctcc	tgcatccaca	180
gcatcttctc	caacaaatat	aaccttgagt	ggcttcttgt	aatctatgtt	ctttgttttc	240
ctaaggactt	ccattgcata	tcctacaata	ttttctctac	gcaccactag	aattaagcag	300
g						301

&lt;210&gt; 273

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

## &lt;400&gt; 273

```

acatgtgtgt atgtgtatct ttgggaaaaa aanaagacat cttgtttayt atttttttgg      60
agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactygaa      120
gaaccgtcta aaaataaaat ttaccatgtc dtatattcct tatagtatgc ttatttcacc      180
ttytttctgt ccagagagag tatcagtgc ananatttma gggagaamac atgmattggt      240
gggacttnty tttacngagm accctgcccc sgcgcctcgc makcngantt ccgcsananc      300
t                                                                                   301

```

&lt;210&gt; 274

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

## &lt;400&gt; 274

```

cttataact cttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg      60
aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa      120
tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttggt gaaaagtcca      180
tctaggtatg gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc      240
aattgtgctt cttttgataa gaagctttct tggatcatatc aggaaattcc aganaaagtc      300
c                                                                                   301

```

&lt;210&gt; 275

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

## &lt;400&gt; 275

```

tcgggtgcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg      60
gggtgaaatt ggccaacttt ctattaactt atgttggcaa ttttgccacc aacagtaagc      120
tggcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtgag      180
tcaagagact cccaggcctc agcgtacctg cccgggcggc cgctcgaagc cgaattctgc      240
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccctat      300
a                                                                                   301

```

&lt;210&gt; 276

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 276

```

tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat      60
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat      120
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc      180
caatacattt aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttctgt      240
aaaactattc agtatgtttc cttgtcttca tgtctgagaa ggctctcctt caatggggat      300
g                                                                                   301

```

&lt;210&gt; 277

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 277  
 tttgttgatg tcagtatttt attacttgcg ttatgagtg tcacctggga aattctaaag 60  
 atacagagga cttggaggaa gcagagcaac tgaatttaat taaaagaag gaaaacattg 120  
 gaatcatggc actcctgata ctttcccaa tcaacactct caatgcccc ccctcgtcct 180  
 caccatagtg gggagactaa agtggccacg gatttgcctt angtgtgcag tgcgttctga 240  
 gttcncctgc gattacatct gaccagtctc ctttttccga agtccttccg ttcaatcttg 300  
 c 301

<210> 278  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 278  
 taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60  
 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120  
 cagtcctctac tggtattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180  
 aatgaacatc tcatgtgtgc tcacaatgtt ctggcactat tataagtgtc tcacagggtt 240  
 tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300  
 c 301

<210> 279  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 279  
 aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60  
 gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120  
 ttagaccttt acctccagc caccacacag tgcttgatat ttcagagtca gtcattgggt 180  
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240  
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300  
 a 301

<210> 280  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 280  
 ggtactggag ttttctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60  
 tagaaagggt gtggaaccaa attgtgggtca atggaaatag gagaatatgg ttctcactct 120  
 tgagaaaaaa acctaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180  
 gtttgatata gtttaggggt ggggttagat taagatctaa attacatcag gacaaaagaga 240  
 cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag 300  
 t 301

<210> 281  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 281  
 aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatatc 60  
 gccgagcaat ccaaattcctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120  
 atgtggtagc aatggcttta tcgggttata cggatgagaa gaactccctt tggagagaaa 180  
 tgtgtagcac actgcgatta cagctaaata acccgattt gtgtgtcatg ttgcatctc 240  
 tgacaagtga aacaggatct tacgatggag ttttgtatga aaacaaagt gcagtacctc 300  
 g 301

<210> 282  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 282  
 caggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60  
 tccagaaccc aaaaatttaag aaattcaaaa agacattttg tgggcacctg ctagcacaga 120  
 agcgcagaag caaagcccag gcagaaccat gctaacctta cagctcagcc tgcacagaag 180  
 cgcaagaagca aagcccaggc agaaccatgc taaccttaca gctcagcctg cacagaagcg 240  
 cagaagcaaa gccccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300  
 a 301

<210> 283  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 283  
 atctgtatac ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaag 60  
 cactttgagg gctttataat aatagtctgc ttgaaaaaa aaatgtgtag ttgatactca 120  
 gtgcactctc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180  
 acttcccagg ttttatgcaa aaattttgtt aaattctata atggtgatat gcatctttta 240  
 ggaaacatat acatttttaa aaatctattt tatgtaagaa ctgacagacg aatttgcttt 300  
 g 301

<210> 284  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 284  
 caggtaaaaa acgctattaa gtggcttaga atttgaacat ttgtggtctt tatttacttt 60  
 gcttcgtgtg tgggcaaagc aacatcttcc ctaaatatat attaccaaga aaagcaagaa 120  
 gcagattagg tttttgacaa aacaaacagg ccaaaagggg gctgacctgg agcagagcat 180  
 ggtgagaggc aaggcatgag agggcaagtt tgttgtggac agatctgtgc ctactttatt 240  
 actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt 300  
 a 301

<210> 285  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

&lt;400&gt; 285

acatcacat	gatcgatcc	cccacccatt	atacgttgta	tgtttacata	aatactcttc	60
aatgatcatt	agtgttttaa	aaaaaatact	gaaaactcct	tctgcatccc	aatctctaac	120
caggaaagca	aatgctattt	acagacctgc	aagccctccc	tcaaacnaaa	ctatttctgg	180
attaaatatg	tctgacttct	tttgaggta	cacgactagg	caaagtctat	ttacgatctg	240
caaaagctgt	ttgaagagtc	aaagccccca	tgtgaacacg	atttctggac	cctgtaacag	300
t						301

&lt;210&gt; 286

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 286

taccactgca	ttccagcctg	ggtgacagag	tgagactccg	tctccaaaaa	aaactttgct	60
tgtatattat	ttttgcctta	cagtggatca	ttctagtagg	aaaggacagt	aagatttttt	120
atcaaaatgt	gtcatgccag	taagagatgt	tatattcttt	tctcatttct	tccccaccca	180
aaaataagct	accatatagc	ttataagtct	caaatttttg	ccttttacta	aaatgtgatt	240
gtttctgttc	attgtgtatg	cttcatcacc	tatattaggc	aaattccatt	ttttcccttg	300
t						301

&lt;210&gt; 287

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 287

tacagatctg	ggaactaaat	attaaaaatg	agtgtggctg	gatatatgga	gaatgttggg	60
cccagaagga	acgtagagat	cagatattac	aacagctttg	ttttgagggt	tagaaatatg	120
aaatgatattg	gttatgaacg	cacagttag	gcagcagggc	cagaatcctg	accctctgcc	180
ccgtggttat	ctcctcccca	gcttggtctg	ctcatgttat	cacagtattc	cattttgttt	240
gttgcatgtc	ttgtgaagcc	atcaagattt	tctcgtctgt	tttctctca	ttggaatgc	300
t						301

&lt;210&gt; 288

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 288

gtacaccta	ctgcaaggac	agctgaggaa	tgtaatgggc	agccgctttt	aaagaagtag	60
agtcaatagg	aagacaaatt	ccagttccag	ctcagctctg	gtatctgcaa	agctgcaaaa	120
gatcttttaa	gacaatttca	agagaatatt	tccttaaagt	tggaatttg	gagatcatac	180
aaaagcatct	gcttttgtga	tttaatttag	ctcatctggc	caactggaaga	atccaaacag	240
tctgccttaa	ttttggatga	atgcatgatg	gaaattcaat	aatttagaaa	gttaaaaaaa	300
a						301

&lt;210&gt; 289

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 289

ggtacactgt	ttccatgtta	tgtttctaca	cattgtctacc	tcagtgtctc	tggaaactta	60
gcttttgatg	tctccaagta	gtccaccttc	atttaactct	ttgaaactgt	atcatctttg	120
cgaagtaaga	gtggtggcct	atttcagctg	ctttgacaaa	atgactggct	cctgacttaa	180

cgttctataa atgaatgtgc tgaagcaaag tgcccatggt ggccggcgaan aagagaaaga 240  
 tgtgttttgt tttggactct ctgtgggtccc ttccaatgct gtgggtttcc aaccagnnga 300  
 a 301

<210> 290  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 290  
 acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac 60  
 tgactgatct gttcatttct ctcacagctc ttacccccaa aagcttttcc accctaagtg 120  
 ttctgacctc cttttctaata cacagtaggg atagaggcag anccacctac aatgaacatg 180  
 gagttctatc aagaggcaga aacagcacag aatcccagtt ttaccattcg ctagcagtgc 240  
 tgccctgaac aaaaacattt ctccatgtct cattttcttc atgcctcaag taacagtgag 300  
 a 301

<210> 291  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 291  
 caggtaccaa tttcttctat cctagaaaca tttcatttta tgttgttgaa acataacaac 60  
 tatatcagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc 120  
 tttactcttt tgtttatagg tgaatcacia aatgtatttt tatgtattct gtatttcaat 180  
 agccatggct gtttacttca ttttaatttat ttagcataaa gacattatga aaaggcctaa 240  
 acatgagctt cacttcccca ctaactaatt agcatctggt atttcttaac cgtaatgcct 300  
 a 301

<210> 292  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 292  
 accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc 60  
 tgtattaaat aatttttaag tttaaaagat aaaataccat cattttaaat gttggtattc 120  
 aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaatgat ttgcnagatg 180  
 ggaaatatag tasttyatga atgttnatta aattccagtt ataatagttg ctacacactc 240  
 tcactacaca cacagacccc acagtcctat atgccacaaa cacatttcca taacttgaaa 300  
 a 301

<210> 293  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 293  
 ggtaccaagt gctggtgccg gcctgttacc tgtttctact gaaaagtctg gctaagtctc 60  
 ttgtgtagtc acttctgatt ctgacaatca atcaatcaat gccctagagc actgactggt 120  
 aacacaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt 180

gtgagaat tttaaaaggc tacttgata ataacccttg tcatttttaa tgtacctcgg 240  
 ccgcgaccac gctaagccga attctgcaga tatccatcac actggcgcc gctcgagcat 300  
 g 301

<210> 294  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 294  
 tgaccataa caatatacac tagctatctt tttactgtc catcattagc accaatgaag 60  
 attcaataaa attaccttta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag 120  
 tttactata gtcacaganc ttaaatattc acattgtttt ctatgtctac tgaaaataag 180  
 ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240  
 cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt 300  
 t 301

<210> 295  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 295  
 gtactctttc tctcccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta 60  
 cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac 120  
 ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180  
 actggtagaa aaactctga agagctagtc tatcagcatc tgacaggtga attggatggg 240  
 tctcagaacc atttcacca gacagcctgt ttctatcctg ttttaataaat tagtttgggt 300  
 tctct 305

<210> 296  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 296  
 aggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct 60  
 cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg 120  
 attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac 180  
 tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt 240  
 tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg 300  
 c 301

<210> 297  
 <211> 300  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(300)  
 <223> n = A,T,C or G

<400> 297  
 actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta 60  
 aaggttttga aaaccttgaa ggagaatcat ttgacaaga agtacttaag agtctagaga 120  
 acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt 180



tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggtc 240  
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc aacttgccg 300

<210> 298

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 298

tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc ccctcccgcg 60  
ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgcccgtg 120  
tgaagctctc agatcaatca cgggaaggcc ctggcggtgg tggccacctg gaaccacct 180  
gtcctgtctg tttacatttc actaycaggt tttctctggg cattacnatt tgttccccta 240  
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcagggtggct ctcagcgagg 300  
t 301

<210> 299

<211> 301

<212> DNA

<213> Homo sapien

<400> 299

gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggctctctgc 60  
tcactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct cccaggtagc 120  
tgggattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg 180  
gagtttcgcc atgttggccca gctggctctca aactcctgac ctcaagcgac ctgcctgcct 240  
cggcctccca aagtgtctgga attataggca tgagtcaaca cgcccagcct aaagatattt 300  
t 301

<210> 300

<211> 301

<212> DNA

<213> Homo sapien

<400> 300

attcagtttt atttctgccc ccagtatctg taaccaggag tgccacaaaa tcttgccaga 60  
tatgtcccac acccactggg aaaggctccc acctggctac ttcctctatc agctgggtca 120  
gctgcattcc acaaggttct cagcctaatt agtttcaact cctgccagtc tcaaaactta 180  
gtaaagcaag accatgacat tccccacgg aaatcagagt ttgccccacc gtcttggttac 240  
tataaagcct gcctctaaca gtccttgctt cttcacacca atcccagcgc catcccccat 300  
g 301

<210> 301

<211> 301

<212> DNA

<213> Homo sapien

<400> 301

ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc 60  
agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttggt 120  
gggaactcac aaagaccctc agagctgaga caccacaaac agtgggagct cacaaagacc 180  
ctcagagctg agacaccac aacagtggga gtcacaaaag accctcagag ctgagacacc 240  
cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300  
t 301

<210> 302

<211> 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 302

```

aggtacacat ttagcttgtg gtaaatgact cacaaaactg attttaaaat caagttaatg      60
tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac      120
ttgagttggt tcttagtatt atttatggta aataggctct taccacttgc aaataactgg      180
ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca      240
caggatttga gatgctaagg cccagagat cgtttgatcc aaccctctta ttttcagagg      300
g                                                                                   301

```

&lt;210&gt; 303

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 303

```

aggtaccaac tgtggaaata ggtagaggat cattttttct ttccatatca actaagttgt      60
atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac      120
tggtcaatgg aactaccgct tgcattgtaa aaatgggtgt ttgtgaaatg atcataggcc      180
agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc      240
catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac      300
c                                                                                   301

```

&lt;210&gt; 304

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 304

```

acatggatgt tattttgcag actgtcaacc tgaatttgta tttgcttgac attgcctaatt      60
tattagtttc agtttcagct taccactttt ttgtctgcaa catgcaraas agacagtgcc      120
cttttttagtg tatcatatca ggaatcatct cacattgggt ttgtgccatta ctgggtgcagt      180
gactttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga      240
ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct      300
c                                                                                   301

```

&lt;210&gt; 305

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 305

```

gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag      60
caggggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggcg      120
taaaggagga gaaacagata caaaatctcc aactcagtat taaggatttc tcatgcctag      180
aatattggta gaaacaagaa tacattcata tggcaataa ctaaccatgg tggaacaaaa      240
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag      300
a                                                                                   301

```

&lt;210&gt; 306

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 306

Val Leu Gly Trp Val Ala Glu Leu

1 5  
 <210> 307  
 <211> 637  
 <212> DNA  
 <213> Homo sapien

<400> 307  
 acaggggratg aagggaaagg gagaggatga ggaagccccc ctgggggattt ggtttggtcc 60  
 ttgtgatcag gtggtctatg gggcttatcc ctacaaagaa gaatccagaa atagggggcac 120  
 attgaggaat gatacttgag cccaaagagc attcaatcat tgttttattt gccttmtttt 180  
 cacaccattg gtgagggagg gattaccacc ctgggggttat gaagatgggt gaacacccca 240  
 cacatagcac cggagatatg agatcaacag tttcttagcc atagagattc acagcccaga 300  
 gcaggaggac gcttgcacac catgcaggat gacatggggg atgctgctcg gattgggtgtg 360  
 aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacggtgggg caaactctga 420  
 tttccgtggg ggaatgtcat ggtcttgctt tactaagttt tgagactggc aggtagtga 480  
 actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatatag gaagtagcca 540  
 ggtgggagcc tttccagtg ggtgtgggac atatctggca agattttgtg gcactcctgg 600  
 ttacagatac tggggcagca aataaaactg aatcttg 637

<210> 308  
 <211> 647  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc feature  
 <222> (1)...(647)  
 <223> n = A,T,C or G

<400> 308  
 acgattttca ttatcatgta aatcgggtca ctcaaggggc caaccacagc tgggagccac 60  
 tgctcagggg aaggttcata tgggactttc tactgcccac gggtctatac aggatataaa 120  
 ggngcctcac agtatagatc tggtagcaaa gaagaagaaa caaacactga tctctttctg 180  
 ccaccctctt gacccttttg aactcctctg accctttaga acaagcctac ctaatatctg 240  
 ctagagaaaa gaccaacaac ggcctcaaag gatctcttac catgaaggtc tcagctaatt 300  
 cttggctaag atgtgggttc cacattagggt tctgaatatg gggggaagg tcaatttgct 360  
 cattttgtgt gtggataaag tcaggatgcc caggggccag agcagggggc tgcttgcttt 420  
 gggaacaatg gctgagcata taaccatagg ttatggggaa caaaacaaca tcaaagtcac 480  
 tgtatcaatt gccatgaaga cttgagggac ctgaatctac cgattcatct taaggcagca 540  
 ggaccagttt gagtggcaac aatgcagcag cagaatcaat ggaaacaaca gaatgattgc 600  
 aatgtccttt ttttctcct gcttctgact tgataaaaagg ggaccgt 647

<210> 309  
 <211> 460  
 <212> DNA  
 <213> Homo sapien

<400> 309  
 actttatagt ttaggctgga cattggaaaa aaaaaaagc cagaacaaca tgtgatagat 60  
 aatatgattg gctgcacact tccagactga tgaatgatga acgtgatgga ctattgtatg 120  
 gagcacatct tcagcaagag ggggaatac tcatcatttt tggccagcag ttgtttgatc 180  
 accaaacatc atgccagaat actcagcaaa ccttcttagc tcttgagaag tcaaagtccg 240  
 ggggaattta ttcctggcaa ttttaattgg actccttatg tgagagcagc ggctaccag 300  
 ctgggggtgt ggagcgaacc cgtcactagt ggacatgcag tggcagagct cctggtaacc 360  
 acctagagga atacacaggc acatgtgtga tgccaagcgt gacacctgta gcactcaaat 420  
 ttgtcttgtt tttgtctttc ggtgtgtaag attcttaagt 460

<210> 310  
 <211> 539  
 <212> DNA  
 <213> Homo sapien

```

<400> 310
acgggactta tcaaataaag ataggaaaag aagaaaactc aaatattata ggcagaaatg      60
ctaaaggttt taaaatatgt caggattgga agaaggcatg gataaagaac aaagttcagt      120
taggaaagag aaacacagaa ggaagagaca caataaaagt cattatgtat tctgtgagaa      180
gtcagaçagt aagattttgtg ggaaatgggt tggtttggtg tatggtatgt atttttagcaa      240
taatctttat ggcagagaaa gctaaaatcc tttagcttgc gtgaatgatc acttgctgaa      300
ttcctcaagg taggcatgat gaaggagggt ttagaggaga cacagacaca atgaactgac      360
ctagatagaa agccttagta tactcagcta ggaatagtga ttctgagggc aactgtgac      420
atgattatgt cattacatgt atggtagtga tggggatgat aggaaggaag aacttatggc      480
atattttcac cccacaaaaa gtcagttaaa tattgggaca ctaaccatcc aggtcaaga      539

```

```

<210> 311
<211> 526
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(526)
<223> n = A,T,C or G

```

```

<400> 311
caaatgtgag ccaatgacat agaattttac aaatcaagaa gcttattctg gggccatttc      60
ttttgacgtt ttctctaaac tactaaagag gcattaatga tccataaatt atattatcta      120
catttacagc atttaaaatg tgttcagcat gaaatattag ctacagggga agctaaataa      180
attaaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg      240
tttttcacaa gtgaagcatt cttataaagt gtcataacct ttttggggaa actatgggaa      300
aaaaatgggga aactctgaag ggttttaagt atcttacctg aagctacaga ctccataacc      360
tctctttaca gggagctcct gcagccccta cagaaatgag tggctgagat tcttgattgc      420
acagcaagag cttctcatct aaaccctttc cttttttagt atctgtgtat caagtataaa      480
agttctataa actgtagtnt acttatttta atcccaaaag cacagt      526

```

```

<210> 312
<211> 500
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(500)
<223> n = A,T,C or G

```

```

<400> 312
cctctctctc cccaccccct gactctagag aactggggtt tctcccagta ctccagcaat      60
tcattttctga aagcagttga gccactttat tccaaagtac actgcagatg ttcaaactct      120
ccattttctct tccccttcca cctgccagtt ttgctgactc tcaacttgtc atgagtgtaa      180
gcattaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg      240
gcttcttagg aaaatatatt tcttccaaaa tcagtaggaa atctaaactt atcccccttt      300
tgcagatgtc tagcagcttc agacatttgg ttaagaaccc atgggaaaaa aaaaaatcct      360
tgctaattgt gtttcctttg taaaccanga ttcttatttg nctggtatag aatatcagct      420
ctgaacgtgt ggtaaagatt tttgtgtttg aatataggag aaatcagttt gctgaaaagt      480
tagtcttaat tatctattgg

```

```

<210> 313
<211> 718
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(718)

```

<223> n = A,T,C or G

<400> 313

ggagatttgt	gtggtttgc	gccgagggag	accaggaaga	tctgcatggt	gggaaggacc	60
tgatgataca	gaggtgagaa	ataagaaagg	ctgctgactt	taccatctga	ggccacacat	120
ctgctgaaat	ggagataatt	aacatcacta	gaaacagcaa	gatgacaata	taatgtctaa	180
gtagtgcacat	gtttttgcac	atttccagcc	cttttaaata	tccacacaca	caggaagcac	240
aaaaggaagc	acagagatcc	ctgggagaaa	tgcccggccg	ccatcttggg	tcatcgatga	300
gcctcgccct	gtgcctgntc	ccgcttgtga	gggaaggaca	ttagaaaatg	aattgatgtg	360
ttccttaaag	gatggcagga	aaacagatcc	tggtgtggat	atattttga	acgggattac	420
agatttgaaa	tgaagtcaca	aagtgagcat	taccaatgag	aggaaaacag	acgagaaaat	480
cttgatgggt	cacaagacat	gcaacaaaca	aaatggaata	ctgtgatgac	acgagcagcc	540
aactggggag	gagataccac	ggggcagagg	tcaggattct	ggccctgctg	cctaactgtg	600
cgttatacca	atcatttcta	tttctaccct	caaacaagct	gtngaatatc	tgacttacgg	660
ttcttntggc	ccacattttc	atnatccacc	ccntcntttt	aannttantc	caaantgt	718

<210> 314

<211> 358

<212> DNA

<213> Homo sapien

<400> 314

gtttattttac	attacagaaa	aaacatcaag	acaatgtata	ctatttcaaa	tatatccata	60
cataatcaaa	tatagctgta	gtacatgttt	tcattggtgt	agattaccac	aaatgcaagg	120
caacatgtgt	agatctcttg	tcttattctt	ttgtctataa	tactgtattg	tgtagtccaa	180
gctctcggtg	gtccagccac	tgtgaaacat	gtccccttta	gattaacctc	gtggacgctc	240
ttgttggtatt	gctgaactgt	agtgcctgt	attttgcttc	tgtctgtgaa	ttctgttgc	300
tctggggcat	ttccttgtga	tgcagaggac	caccacacag	atgacagcaa	tctgaatt	358

<210> 315

<211> 341

<212> DNA

<213> Homo sapien

<400> 315

taccacctcc	ccgctggcac	tgatgagccg	catcaccatg	gtcaccagca	ccatgaaggc	60
ataggtgatg	atgaggacat	ggaatgggcc	cccaaggatg	gtctgtccaa	agaagcgagt	120
gacccccatt	ctgaagatgt	ctggaacctc	taccagcagg	atgatgatag	ccccaatgac	180
agtcaccagc	tccccgacca	gccggatata	gtccttaggg	gtcatgtagg	cttctctgaag	240
tagcttctgc	tgtaaagagg	tggtgtcccg	ggggctcgtg	cggttattgg	tcctgggctt	300
gagggggcgg	tagatgcagc	acatggtgaa	gcagatgatg	t		341

<210> 316

<211> 151

<212> DNA

<213> Homo sapien

<400> 316

agactgggca	agactcttac	gccccacact	gcaatttggt	cttggtgcog	tatccattta	60
tgtgggcctt	tctcgagttt	ctgattataa	acaccactgg	agcgatgtgt	tgactggact	120
cattcaggga	gctctgggtg	caatattagt	t			151

<210> 317

<211> 151

<212> DNA

<213> Homo sapien

<400> 317

agaactagt	gacctaata	aaataacctga	aacatatatt	ggcattttatc	aatggctcaa	60
atcttcattt	atctctggcc	ttaacctctgg	ctcctgaggg	tgcgccagc	agatcccagg	120
ccagggctct	gttcttgcca	cacctgcttg	a			151

<210> 318  
<211> 151  
<212> DNA  
<213> Homo sapien

<400> 318  
actggtggga ggcgctgttt agttggctgt tttcagaggg gtctttcgga gggacctcct 60  
gctgcaggct ggagtgtctt tttcctggc gggagaccgc acattccact gctgaggctg 120  
tgggggcggt ttatcaggca gtgataaaca t 151

<210> 319  
<211> 151  
<212> DNA  
<213> Homo sapien

<400> 319  
aactagtga tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta 60  
catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg 120  
taagattggg tttatgtgat tttagtgggt a 151

<210> 320  
<211> 150  
<212> DNA  
<213> Homo sapien

<400> 320  
aactagtga tccactagtc cagtgtggtg gaattccatt gtgttggggt tctagatcgc 60  
gagcggtgc cctttttttt tttttttttg ggggggaatt tttttttttt aatagttatt 120  
gagtgttcta cagcttacag taaataccat 150

<210> 321  
<211> 151  
<212> DNA  
<213> Homo sapien

<400> 321  
agcaactttg tttttcatcc aggttathtt aggccttagga tttcctctca cactgcagtt 60  
taggggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg 120  
tgcctctgag aaatcaaagt cttcatacac t 151

<210> 322  
<211> 151  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)..(151)  
<223> n = A,T,C or G

<400> 322  
atccagcatc ttctcctgtt tcttgcttc cttttcttc ttcttasatt ctgcttgagg 60  
tttgggcttg gtcagtttgc cacagggtt ggagatggtg acagtcttct ggcattcggc 120  
attgtgcagg gctcgttca nacttcagt t 151

<210> 323  
<211> 151  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature

96

&lt;222&gt; (1)...(151)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 323

tgaggacttg	tkttcttttt	ctttattttt	aatcctctta	ckttgtaa	atattgccta	60
nagactcant	tactacccag	tttgtggtt	twtgaggagaa	atgtaactgg	acagttagct	120
gttcaatyaa	aaagacactt	ancccatgtg	g			151

&lt;210&gt; 324

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(461)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 324

acctgtgtgg	aatttcagct	ttcctcatgc	aaaaggattt	tgtatccccg	gcctacttga	60
agaagtggtc	agctaaagga	atccagggtg	ttgggtggac	tgtaataacc	tttcatgaaa	120
agagttacta	cgaatcccat	cttggttcca	gctatatcac	tgacagcatg	gtagaagact	180
gcgaacctca	cttctagact	ttcacgggtg	gacgaaacgg	gttcagaaac	tgccaggggc	240
ctcatacagg	gatatacaaa	taccttttgt	gctacccagg	ccctggggaa	tcagggtgact	300
cacacaaatg	caatagttgg	tcaactgcatt	tttacctgaa	ccaaagctaa	acccgggtgtt	360
gccaccatgc	accatggcat	gccagagttc	aacactgttg	ctcttgaaaa	ttgggtctga	420
aaaaacgcac	aagagcccct	gccctgccct	agctgangca	c		461

&lt;210&gt; 325

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 325

acactgtttc	catgttatgt	ttctacacat	tgtacacctca	gtgctcctgg	aaacttagct	60
tttcatgtct	ccaagtagtc	caccttcatt	taactctttg	aaactgtatc	atctttgcca	120
agtaagagtg	gtggcctatt	tcagctgctt	tgacaaaaatg	actggctcct	gacttaacgt	180
tctataaatg	aatgtgctga	agcaaaagtgc	ccatgggtggc	ggcgaagaag	agaaagatgt	240
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&lt;210&gt; 326

&lt;211&gt; 1215

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 326

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<210> 327  
 <211> 220  
 <212> PRT  
 <213> Homo sapien

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<400> 327
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Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
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Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
35     40     45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
50     55     60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
65     70     75     80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
85     90     95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
100    105    110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
115    120    125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
130    135    140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
145    150    155    160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
165    170    175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
180    185    190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
195    200    205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
210    215    220

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<210> 328  
 <211> 234  
 <212> DNA  
 <213> Homo sapien

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<400> 328
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atccgcagtg ggtgctgtca gccacacact gtttcagaa ctctacacc atcgggctgg      180
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<210> 329  
 <211> 77  
 <212> PRT  
 <213> Homo sapien

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<400> 329
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1      5      10      15

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                   20                  25                  30  
 Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr  
                   35                  40                  45  
 His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu  
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 Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala  
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<210> 330  
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 <212> DNA  
 <213> Homo sapien

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<210> 331  
 <211> 22  
 <212> PRT  
 <213> Homo sapien

<400> 331  
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 Val Ser Gly Ser Cys Ser  
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<210> 332  
 <211> 2507  
 <212> DNA  
 <213> Homo sapien

<400> 332  
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&lt;210&gt; 333

&lt;211&gt; 3030

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 333

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&lt;210&gt; 334

&lt;211&gt; 2417

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 334

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&lt;210&gt; 335

&lt;211&gt; 2984

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 335

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tctttacatt	tcttttaaaa	taagcattta	gtgctcagtc	cctactgagt	actctttctc	2520
tcccctcctc	tgaattttaat	tctttcaact	tgcaatttgc	aaggattaca	catttcactg	2580
tgatgtatat	tgtgttgcaa	aaaaaaaaaa	aagtgtcttt	gtttaaaatt	acttggtttg	2640
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ccatttcacc	cagacagcct	gtttctatcc	tgtttaataa	attagtttgg	gttctctaca	2820
tgcataacaa	accctgtccc	aatctgtcac	ataaaagtct	gtgactgaa	gtttagtcag	2880
cacccccacc	aaactttatt	tttctatgtg	tttttgcaca	catatgagtg	ttttgaaaat	2940
aaagtaccca	tgtctttatt	agaaaaaaaa	aaaaaaaaaa	aaaa		2984

&lt;210&gt; 336

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 336

Pro Ser Phe Pro Thr Leu Leu Ser Arg Arg His Leu Gly Ser Tyr Leu

102

```

      1           5           10           15
Leu Asp Ser Glu Asn Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr
      20           25           30
Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln
      35           40           45
Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala
      50           55           60
Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln
      65           70           75           80
Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
      85           90           95
Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala
      100          105          110
Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn
      115          120          125
Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro
      130          135          140
Ala Phe Trp
145

```

```

<210> 337
<211> 9
<212> PRT
<213> Homo sapien

```

```

<400> 337
Ala Leu Thr Gly Phe Thr Phe Ser Ala
1           5

```

```

<210> 338
<211> 9
<212> PRT
<213> Homo sapien

```

```

<400> 338
Leu Leu Ala Asn Asp Leu Met Leu Ile
1           5

```

```

<210> 339
<211> 318
<212> PRT
<213> Homo sapien

```

```

<400> 339
Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Pro Phe Leu
1           5           10           15
Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
      20           25           30
Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
      35           40           45
Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
      50           55           60
Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
      65           70           75           80
Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
      85           90           95
Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
      100          105          110
Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
      115          120          125
Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met

```

130	135	140
His Ile Gly Val Asn	His Leu Gly His Phe Leu	Leu Thr His Leu Leu
145	150	155
Leu Glu Lys Leu Lys	Glu Ser Ala Pro Ser Arg	Ile Val Asn Val Ser
165	170	175
Ser Leu Ala His His	Leu Gly Arg Ile His Phe	His Asn Leu Gln Gly
180	185	190
Glu Lys Phe Tyr Asn	Ala Gly Leu Ala Tyr Cys	His Ser Lys Leu Ala
195	200	205
Asn Ile Leu Phe Thr	Gln Glu Leu Ala Arg Arg	Leu Lys Gly Ser Gly
210	215	220
Val Thr Thr Tyr Ser	Val His Pro Gly Thr Val	Gln Ser Glu Leu Val
225	230	235
Arg His Ser Ser Phe	Met Arg Trp Met Trp Trp	Leu Phe Ser Phe Phe
245	250	255
Ile Lys Thr Pro Gln	Gln Gly Ala Gln Thr Ser	Leu His Cys Ala Leu
260	265	270
Thr Glu Gly Leu Glu	Ile Leu Ser Gly Asn His	Phe Ser Asp Cys His
275	280	285
Val Ala Trp Val Ser	Ala Gln Ala Arg Asn Glu	Thr Ile Ala Arg Arg
290	295	300
Leu Trp Asp Val Ser	Cys Asp Leu Leu Gly Leu	Pro Ile Asp
305	310	315

<210> 340  
 <211> 483  
 <212> DNA  
 <213> Homo sapien

<400> 340  
 gccgaggtct gccttcacac ggaggacacg agactgcttc ctcaagggtc cctgcctgcc 60  
 tggacactgg tgggaggcgc tgtttagttg gctgttttca gaggggtctt tcggagggac 120  
 ctctgctgctc aggtctggagt gtctttattc ctggcgaggag accgcacatt ccactgctga 180  
 gggtgtgggg gcggtttatc aggcagtgat aaacataaga tgtcatttcc ttgactccgg 240  
 ccttcaattt tctctttggc tgacgacgga gtccgtggtg tcccgatgta actgacccct 300  
 gctccaaacg tgacatcact gatgctcttc tcgggggtgc tgatggcccg cttggtcacg 360  
 tgcacaatct cgccattcga ctcttgctcc aaactgtatg aagacacctg actgcacgtt 420  
 tttctggggc ttccagaatt taaagtgaag ggcagcactc ctaagctccg actccgatgc 480  
 ctg 483

<210> 341  
 <211> 344  
 <212> DNA  
 <213> Homo sapien

<400> 341  
 ctgctgctga gtcacagatt tcattataaa tagcctccct aaggaaaata cactgaatgc 60  
 tatttttact aaccattcta tttttataga aatagctgag agtttctaaa ccaactctct 120  
 gctgccttac aagtattaaa tattttactt ctttccataa agagtagctc aaaatatgca 180  
 attaatttaa taatttctga tgatggtttt atctgcagta atatgtatat catctattag 240  
 aatttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc 300  
 ctgattctta acattgtctt taatgaccac aagacaacca acag 344

<210> 342  
 <211> 592  
 <212> DNA  
 <213> Homo sapien

<400> 342  
 acagcaaaaa agaaactgag aagcccaaty tgctttcttg ttaacatcca cttatccaac 60  
 caatgtggaa acttcttata cttggttcca ttatgaagtt ggacaattgc tgctatcaca 120  
 cctggcaggt aaaccaatgc caagagagtg atggaaacca ttggcaagac tttgttgatg 180

104

```

accaggattg gaattttata aaaatattgt tgatgggaag ttgctaaagg gtgaattact 240
tccctcagaa gagtgtaaag aaaagtcaga gatgctataa tagcagctat ttttaattggc 300
aagtgccact gtggaaagag ttcctgtgtg tgctgaagtt ctgaaggcca gtcaaattca 360
tcagcatggg ctgttttggtg caaatgcaaa agcacagggtc tttttagcat gctggctctct 420
cccgtgtcct tatgcaaata atcgtcttct tctaaatttc tcctaggctt cattttccaa 480
agttcttctt ggtttgatgt gtcttttctg ctttccatta attctataaa atagtatggc 540
ttcagccacc cactcttcgc cttagcttga ccgtgagttc cggctgccgc tg 592

```

&lt;210&gt; 343

&lt;211&gt; 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 343

```

ttcttgacct cctcctcctt caagctcaaa caccacctcc cttattcagg accggcactt 60
cttaattgtt gtggctttct ctccagcctc tcttaggagg ggtaatggtg gagttggcat 120
cttgtaactc tcctttctcc tttcttcccc ttctctgcc cgctttccc atcctgctgt 180
agacttcttg attgtcagtc tgtgtcacat ccagtgattg ttttggtttc tgttcccttt 240
ctgactgccc aaggggctca gaaccccagc aatcccttcc tttcactacc ttcttttttg 300
ggggtagttg gaagggactg aaattgtggg gggaaggtag gaggcacatc aataaaggag 360
aaaccaccaa gctgaaaaaa aa 382

```

&lt;210&gt; 344

&lt;211&gt; 536

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 344

```

ctgggcctga agctgtaggg taaatcagag gcaggcttct gagtgatgag agtcctgaga 60
caataggcca cataaacttg gctggatgga acctcacaat aaggtgggtc cctcttggtt 120
gtttaggggg atgccaagga taaggccagc tcagttatat gaagagaagc agaacaaaca 180
agtctttcag agaaatggat gcaatcagag tgggatcccg gtcacatcaa ggtcacactc 240
caccttcagtg tgctgaatg gttgccaggt cagaaaaatc cacccttac gagtgcggt 300
tcgaccctat atccccgcc cgcgctcctt tctccataaa attcttctta gtagctatta 360
ccttcttatt atttgatcta gaaattgcc tctttttacc cctaccatga gccctacaaa 420
caactaacct gccactaata gttatgtcat ccctcttatt aatcatcatc ctagccctaa 480
gtctggccta tgagtgacta caaaaaggat tagactgagc cgaataacaa aaaaaa 536

```

&lt;210&gt; 345

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 345

```

accttttgag gtctctctca ccacctccac agccaccgtc accgtgggat gtgctggatg 60
tgaatgaage ccccatcttt gtgcctcctg aaaagagagt ggaagtgtcc gaggactttg 120
gcgtgggcca ggaaatcaca tctacactg cccaggagcc agacacattt atggaacaga 180
aaataacata tcggaatttg agagacactg ccaactggct ggagattaat ccggacactg 240
gtgccatttc c 251

```

&lt;210&gt; 346

&lt;211&gt; 282

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(282)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 346

```

cgcgtctctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt 60

```

```

ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcaagtaca aattctggga      120
agggagacta tacctggctc ttgccctaag tgagaggtct tccctcccgc accaaaaaat      180
agaaaggctt tctatttcac tggcccaggt agggggaagg agagtaactt tgagtctgtg      240
ggtctcattt cccaaggtgc cttcaatgct catnaaaacc aa                          282

```

&lt;210&gt; 347

&lt;211&gt; 201

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(201)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 347

```

acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca      60
taaataatac ttttaaaaaa ntactancag cttttaccta ngctcctaaa tgcttgtaaa      120
tctgagactg actggacca cccagacca gggcaaagat acatgttacc atatcatctt      180
tataaagaat ttttttttgt c                          201

```

&lt;210&gt; 348

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 348

```

ctgttaatca caacatttgt gcatacttg tgccaagtga gaaaatgttc taaaatcaca      60
agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgcccctg ggcaggcaga      120
aggagacact cccagcatgg aggagggttt atcttttcat cctaggtcag gtctacaatg      180
ggggaagggt ttattataga actcccaaca gccacctca ctctgccac ccacccgatg      240
gccctgcctc c                          251

```

&lt;210&gt; 349

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 349

```

taaaaatcaa gccatttaat tgtatctttg aaggtaaaca atatatggga gctggatcac      60
aacccttgag gatgccagag ctatgggtcc agaactagg gtggtattat caacagagtt      120
cagaagggtc tgaactctac gtgtaccag agaacataat gcaattcatg cattccactt      180
agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca      240
actcctggtt t                          251

```

&lt;210&gt; 350

&lt;211&gt; 908

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 350

```

ctggacactt tgcgagggtt tttgctggct gctgctgctg cccgtcatgc tactcatcgt      60
agcccgcccg gtgaagctcg ctgctttccc tacctcctta agtgactgcc aaacgccac      120
cggtcgaat tgctctggtt atgatgacag agaaaaatgat ctcttcctct gtgacaccaa      180
cacctgtaaa ttgatgggg aatgtttaag aattggagac actgtgactt gcgtctgtca      240
gttcaagtgc aacaatgact atgtgcctgt gtgtggctcc aatggggaga gctaccagaa      300
tgagtgttac ctgcgacagg ctgcatgcaa acagcagagt gagatacttg tgggtgtcaga      360
aggatcatgt gccacagtcc atgaaggctc tggagaaaact agtcaaaagg agacatccac      420
ctgtgatatt tgccagtttg gtgcagaatg tgacgaagat gccgaggatg tctggtgtgt      480
gtgtaatat gactgttctc aaaccaactt caatcccctc tgcgcttctg atgggaaatc      540
ttatgataat gcatgccaaa tcaaagaagc atcgtgtcag aaacaggaga aaattgaagt      600
catgtctttg ggtcgatgtc aagataaac aactacaact actaagtctg aagatgggca      660

```



106

ttatgcaaga	acagattatg	cagagaatgc	taacaaatta	gaagaaagt	ccagagaaca	720
ccacatacct	tgtccggaac	attacaatgg	cttctgcatg	catgggaagt	gtgagcattc	780
tatcaatatg	caggagccat	cttgccagtg	tgatgctggt	tatactggac	aacactgtga	840
aaaaaaggac	tacagtgttc	tatacgttgt	tcccggtcct	gtacgatttc	agtatgtctt	900
aatcgacag						908

&lt;210&gt; 351

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 351

ccagttat	gcaagtgg	agagcctatt	taccataaat	aataactaaga	accaactcaa	60
gtcaaacctt	aatgccattg	ttattgtgaa	ttaggattaa	gtagtaattt	tcaaaattca	120
cattaacttg	attttaaaat	cagwtttgyg	agtcatttac	cacaagctaa	atgtgtacac	180
tatgataaaa	acaaccattg	tattcctgtt	tttctaataa	gtcctaattt	ctaactctgt	240
atatacctt	cgacatcaat	gaactttgtt	ttcttttact	ccagtaataa	agtaggcaca	300
gatctgtcca	caacaaactt	gccctctcat	gccttgccctc	tcaccatgct	ctgctccagg	360
tcagccccct	tttggcctgt	ttgttttgtc	aaaaacctaa	tctgcttctt	gcttttcttg	420
gtaatatata	tttagggaag	atgttgcttt	gcccacacac	gaagcaaagt	aa	472

&lt;210&gt; 352

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 352

ctcaaagcta	atctctcggg	aatcaaacca	gaaaagggca	aggatcttag	gcatgggtgga	60
tgtggataag	gccaggtcaa	tggtctgaag	catgcagaga	aagaggtaca	tcggagcgtg	120
caggctgcgt	tccgtcctta	cgatgaagac	cacgatgcag	tttccaaaca	ttgccactac	180
atacatggaa	aggaggggga	agccaaccca	gaaatgggct	ttctctaatac	ctgggatacc	240
aataagcaca	a					251

&lt;210&gt; 353

&lt;211&gt; 436

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 353

tttttttttt	tttttttttt	tttttttaca	caatgcagtc	atatttttat	tgagtatgtg	60
cacattatgg	tattattact	atactgatta	tatttatcat	gtgacttcta	attaraaaat	120
gtatccaaaa	gcaaaacagc	agatatataa	aattaaagag	acagaagata	gacattaaca	180
gataaggcaa	cttatacatt	gacaatccaa	atccaatata	tttaaactt	tgaggaaatga	240
gggggacaaa	tggaagccar	atcaaatttg	tgtaaaacta	ttcagtatgt	ttcccttgct	300
tcatgtctga	raaggctctc	ccttcaatgg	ggatgacaaa	ctccaaatgc	cacacaaatg	360
ttaacagaat	actagattca	cactggaacg	gggtgaaaga	agaaattatt	ttctataaaa	420
gggtccttaa	tgtagt					436

&lt;210&gt; 354

&lt;211&gt; 854

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 354

ccttttctag	ttcaccagtt	ttctgcaagg	atgctgggta	gggagtgtct	gcaggaggag	60
caagtctgaa	accaaatacta	ggaacatag	gaaacgagcc	aggcacaggg	ctgggtggcc	120
atcagggacc	accctttggg	ttgatatttt	gcttaatctg	catcttttga	gtaagatcat	180
ctggcagtag	aagctgttct	ccaggtacat	ttctctagct	catgtacaaa	aacatcctga	240
aggactttgt	caggtgcctt	gctaaaagcc	agatgcgttc	ggcacttcct	tggtctgagg	300
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gtgagtga	gatccccatt	ataggagcac	ttgggagaga	tcatataaaa	gctgactctt	420
gagtacatgc	agtaatgggg	tagatgtgtg	tggtgtgtct	tcattcctgc	aagggtgctt	480

gtagggagt	gtttccagga	ggaacaagtc	tgaaccaat	catgaaataa	atggtaggtg	540
tgaactggaa	aactaattca	aaagagagat	cgtgatatca	gtgtggttga	tacaccttgg	600
caatatggaa	ggctctaatt	tgcccatatt	tgaataata	attcagcttt	ttgtaataca	660
aaataacaaa	ggattgagaa	tcatggtgtc	taatgtataa	aagacccagg	aaacataaat	720
atatcaactg	cataaatgta	aaatgcatgt	gacccaagaa	ggccccaag	tggcagacaa	780
cattgtaccc	attttccctt	ccaaaatgtg	agcggcgggc	ctgctgcttt	caaggctgtc	840
acacgggatg	tcag					854

&lt;210&gt; 355

&lt;211&gt; 676

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 355

gaaattaagt	atgagctaaa	ttccctgtta	aaacctctag	gggtgacaga	tctcttcaac	60
cagggtcaaag	ctgatctttc	tggaatgtca	ccaaccaagg	gcctatatatt	atcaaaagcc	120
atccacaagt	cataacctga	tgtcagcgaa	gagggcacgg	aggcagcagc	agccactggg	180
gacagcatcg	ctgtaaaaag	cctaccaatg	agagctcagt	tcaaggcgaa	ccacccttc	240
ctgttcttta	taaggcacac	tcataccaac	acgatcctat	tctgtggcaa	gcttgccctc	300
ccctaatacag	atgggggttga	gtaaggctca	gagttgcaga	tgaggtgcag	agacaatcct	360
gtgactttcc	cacggccaaa	aagctgttca	cacctcacgc	acctctgtgc	ctcagtttgc	420
tcactctgcaa	aataaggtcta	ggatttcttc	caaccatttc	atgagttgtg	aagctaaggc	480
tttgtaatac	atggaaaaag	gtagacttat	gcagaaaagc	tttctggctt	tcttatctgt	540
ggtgtctcat	ttgagtgtctg	tccagtgcac	tgatcaagtc	aatgagtaaa	attttaaggg	600
attagatttt	cttgacttgt	atgtatctgt	gagatcttga	ataagtgacc	tgacatctct	660
gcttaaagaa	aaccag					676

&lt;210&gt; 356

&lt;211&gt; 574

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 356

tttttttttt	tttttcagga	aaacattctc	ttactttatt	tgcatctcag	caaaggttct	60
catgtggcac	ctgactggca	tcaaaccaaa	gttcgtaggc	caacaaagat	gggccactca	120
caagcttccc	attttagat	ctcagtgcct	atgagtatct	gacacctgtt	cctctcttca	180
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ttcttctgtc	tctgcctaga	ctggaataaa	aagccaatct	ctctcgtggc	acagggaagg	420
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&lt;210&gt; 357

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 357

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atagatataa	ttattccagt	ttttttaaaa	cttaaaaarat	attccattgc	cgaattaara	240
araarataag	tggtatatgg	aaagaagggc	attcaagcac	actaaaraaa	cctgaggkaa	300
gcataatctg	tacaaaatta	aactgtcctt	tttggcattt	taacaaattt	gcaacgktct	360
tttttttctt	tttctgtttt	tttttttttt	tac			393

&lt;210&gt; 358

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 358

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caagccagag	gttcctccac	aacaaccagt				630

&lt;210&gt; 359

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 359

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atggcattcc	ccaagggaaa	tagagagatt	cttctggatt	atgttcaata	tttatttcac	240
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aacaaaaagc	tcacaccaaa	caaaaccatc	aacttatttt	gtattctata	acatacgaga	600
ctgtaaaagt	gtgacagtgt					620

&lt;210&gt; 360

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 360

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tactcatcat	ttttggccag	cagttgtttg	atcaccaaac	atcatgccag	aatactcagc	180
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agtgagacatg	cagtggcaga	gctcctggta	accacctaga	ggaatacaca	ggcacatgtg	360
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agattcttag	t					431

&lt;210&gt; 361

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 361

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&lt;210&gt; 362

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 362

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cacacttgca cacattctcc ctgataagca cgatgggtg gacaggaagg aaggatttca	420
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&lt;210&gt; 363

&lt;211&gt; 653

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1) ... (653)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 363

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ctcttgngga ttctgggtga catcttcatg aatggcaacc gtgccagwga ggctgtcctc	120
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&lt;210&gt; 364

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 364

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acgtgcatag taaatcttta tatttgctat ggcgttgac tagaggactt ggactgcaac	360
aagtggatgc gcggaaaatg aaatcttctt caatagccca g	401

&lt;210&gt; 365

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 365

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taccagagca tcaagtctct gcagcaggtc attcttgggt aaagaaatga cttccacaaa	180
ctctccatcc cctggctttg gcttcggcct tgcgttttcg gcatcatctc cgtaaatggt	240
gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga	300
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<210> 366  
 <211> 1851  
 <212> DNA  
 <213> Homo sapien

<400> 366

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<210> 367  
 <211> 668  
 <212> DNA  
 <213> Homo sapien

<400> 367

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aaaaaaaa						668

<210> 368  
 <211> 1512  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 368

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taaaaaacag	taatagatac	gaggtgatgc	gcctgtcagt	ggcaagggtt	aagatatttc	1500
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&lt;210&gt; 369

&lt;211&gt; 1853

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 369

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112

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&lt;210&gt; 370

&lt;211&gt; 2184

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 370

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&lt;210&gt; 371

&lt;211&gt; 1855

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1855)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 371

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&lt;210&gt; 372

&lt;211&gt; 1059

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 372

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&lt;210&gt; 373

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 373

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114

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&lt;210&gt; 374

&lt;211&gt; 2000

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 374

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&lt;210&gt; 375

<211> 2040  
 <212> DNA  
 <213> Homo sapien

<400> 375

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<210> 376  
 <211> 329  
 <212> PRT  
 <213> Homo sapien

<400> 376

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Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu
 20          25          30
Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
 35          40          45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
 50          55          60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
 65          70          75          80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
 85          90          95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
100          105          110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
115          120          125

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Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp  
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 Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser  
 145 150 155 160  
 Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys  
 165 170 175  
 Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala  
 180 185 190  
 Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly  
 195 200 205  
 Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr  
 210 215 220  
 Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr  
 225 230 235 240  
 Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu  
 245 250 255  
 Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys  
 260 265 270  
 Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu  
 275 280 285  
 Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu  
 290 295 300  
 Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu  
 305 310 315 320  
 Ser Met Leu Phe Leu Val Ile Ile Met  
 325

&lt;210&gt; 377

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(148)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 377

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 35 40 45  
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu  
 50 55 60  
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp  
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 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp  
 85 90 95  
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro  
 100 105 110  
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp  
 115 120 125  
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser  
 130 135 140  
 Lys Asn Lys Val  
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&lt;210&gt; 378

&lt;211&gt; 1719

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 378

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Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35          40          45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50          55          60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65          70          75          80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85          90          95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
100          105          110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
115          120          125
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
130          135          140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145          150          155          160
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
165          170          175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
180          185          190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
195          200          205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
210          215          220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
225          230          235          240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
245          250          255
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
260          265          270
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
275          280          285
Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
290          295          300
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
305          310          315          320
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
325          330          335
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
340          345          350
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
355          360          365
Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
370          375          380
Pro Arg Thr His Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser
385          390          395          400
Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys
405          410          415
Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly
420          425          430
Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys
435          440          445
Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly
450          455          460
Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys

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465 470 475 480  
 Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys  
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 Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp  
 500 505 510  
 Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu  
 515 520 525  
 Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp  
 530 535 540  
 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln  
 545 550 555 560  
 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val  
 565 570 575  
 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn  
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 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu  
 595 600 605  
 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp  
 610 615 620  
 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys  
 625 630 635 640  
 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys  
 645 650 655  
 Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys  
 660 665 670  
 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala  
 675 680 685  
 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly  
 690 695 700  
 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser  
 705 710 715 720  
 Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser  
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 His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln  
 740 745 750  
 Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys  
 755 760 765  
 Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser  
 770 775 780  
 Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp  
 785 790 795 800  
 Arg Glu Val Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly  
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 Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn  
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 Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe  
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 Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser  
 850 855 860  
 Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn  
 865 870 875 880  
 Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Ser Gln Arg Leu  
 885 890 895  
 Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile  
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 Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn  
 915 920 925  
 Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro  
 930 935 940  
 Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu  
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 Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe

965 970 975  
 Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His  
 980 985 990  
 Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser  
 995 1000 1005  
 Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu  
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 Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His  
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 Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys  
 1075 1080 1085  
 Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr  
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 Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys  
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 Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp  
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 Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His  
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 Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys  
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 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr  
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 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly  
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 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn  
 1445 1450 1455  
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser

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 1475 1480 1485  
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu  
 1490 1495 1500  
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys  
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 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser  
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 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser  
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 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe  
 1570 1575 1580  
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe  
 1585 1590 1595 160  
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly  
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 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Phe Pro  
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 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln  
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 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser  
 1665 1670 1675 168  
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn  
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 Met Lys His Gln Ser Gln Leu  
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&lt;210&gt; 379

&lt;211&gt; 656

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 379

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 35 40 45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
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 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65 70 75 80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
 85 90 95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
 100 105 110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
 115 120 125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
 130 135 140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 145 150 155 160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala  
 165 170 175

Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
 180 185 190  
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr  
 195 200 205  
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met  
 210 215 220  
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn  
 225 230 235 240  
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 245 250 255  
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 260 265 270  
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 275 280 285  
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His Val  
 340 345 350  
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile  
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 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu  
 370 375 380  
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys  
 385 390 395 400  
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu  
 405 410 415  
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn  
 420 425 430  
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro  
 435 440 445  
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu  
 450 455 460  
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu  
 465 470 475 480  
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp  
 485 490 495  
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu  
 500 505 510  
 Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys  
 515 520 525  
 Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly  
 530 535 540  
 Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser  
 545 550 555 560  
 Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr  
 565 570 575  
 His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln  
 580 585 590  
 Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln  
 595 600 605  
 Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys  
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 Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu  
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<211> 671  
 <212> PRT  
 <213> Homo sapien

<400> 380

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			20					25					30		
Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp
			35				40					45			
His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp
	50					55					60				
Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val
	65				70					75				80	
Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn
				85					90					95	
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser
			100					105					110		
Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe
			115				120					125			
Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His
	130					135					140				
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met
	145				150					155				160	
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala
				165					170					175	
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu
			180					185					190		
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr
		195					200					205			
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met
	210					215					220				
Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn
					230					235				240	
Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys
				245					250					255	
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His	Gly
			260					265					270		
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val
		275					280					285			
Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	Leu	Asp	Arg	Tyr
		290				295					300				
Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile
					310					315				320	
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu
					325				330					335	
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val
			340					345					350		
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile
		355					360					365			
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu
		370				375					380				
Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly	Ser	Glu	Asn	Ser	Gln	Pro	Glu	Lys
					390					395				400	
Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Gly	Asp	Arg	Glu	Val	Glu
				405					410					415	
Glu	Glu	Met	Lys	Lys	His	Glu	Ser	Asn	Asn	Val	Gly	Leu	Leu	Glu	Asn
			420					425					430		
Leu	Thr	Asn	Gly	Val	Thr	Ala	Gly	Asn	Gly	Asp	Asn	Gly	Leu	Ile	Pro
		435					440					445			
Gln	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Asn	Gln	Gln	Phe	Pro	Asp	Asn	Glu

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Ser Glu Glu Tyr His	Arg Ile Cys Glu Leu Val	Ser Asp Tyr Lys Glu		
465	470	475	480	
Lys Gln Met Pro Lys	Tyr Ser Ser Glu Asn Ser	Asn Pro Glu Gln Asp		
	485	490	495	
Leu Lys Leu Thr Ser	Glu Glu Glu Ser Gln Arg	Leu Glu Gly Ser Glu		
	500	505	510	
Asn Gly Gln Pro Glu	Lys Arg Ser Gln Glu Pro	Glu Ile Asn Lys Asp		
	515	520	525	
Gly Asp Arg Glu Leu	Glu Asn Phe Met Ala Ile	Glu Glu Met Lys Lys		
	530	535	540	
His Gly Ser Thr His	Val Gly Phe Pro Glu Asn	Leu Thr Asn Gly Ala		
545	550	555	560	
Thr Ala Gly Asn Gly	Asp Asp Gly Leu Ile Pro	Pro Arg Lys Ser Arg		
	565	570	575	
Thr Pro Glu Ser Gln	Gln Phe Pro Asp Thr	Glu Asn Glu Glu Tyr His		
	580	585	590	
Ser Asp Glu Gln Asn	Asp Thr Gln Lys Gln Phe	Cys Glu Glu Gln Asn		
	595	600	605	
Thr Gly Ile Leu His	Asp Glu Ile Leu Ile His	Glu Glu Lys Gln Ile		
	610	615	620	
Glu Val Val Glu Lys	Met Asn Ser Glu Leu Ser	Leu Ser Cys Lys Lys		
625	630	635	640	
Glu Lys Asp Ile Leu	His Glu Asn Ser Thr	Leu Arg Glu Glu Ile Ala		
	645	650	655	
Met Leu Arg Leu Glu	Leu Asp Thr Met	Lys His Gln Ser Gln Leu		
	660	665	670	

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 <212> DNA  
 <213> Homo sapien

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 ccaatatccc aggagaagca ttggggaggt gggggcaggt gaaggacca ggactcacac 180  
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gttatgaaga tggttgaaca cccacacat agcaccggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgctgc acaccatgca ggatgacatg 2940
ggggatgcgc tcgggatttg tgtgaagaag caaggactgt tagaggcagg ctttatagta 3000
acaagacggt ggggcaaact ctgatttccg tgggggaatg tcatggtctt gctttactaa 3060
gttttgagac tggcaggtag tgaaactcat taggctgaga acctgttggg atgcagctga 3120
cccagctgat agaggagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtttt 3279

```

&lt;210&gt; 383

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 383 ..

```

Met Ala Gly Val Arg Asp Glu Gly Gln Gly Ala Arg Trp Pro His Thr
          5                      10                      15

```

```

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
          20                      25                      30

```

```

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
          35                      40                      45

```

```

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
          50                      55                      60

```

```

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
          65                      70                      75                      80

```

```

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala

```

125

	85		90		95										
Trp	Ala	Leu	Thr	Gln	Pro	Pro	Ser	Gln	Ser	Pro	Gly	Pro	Gln	Ser	Leu
	100							105					110		
Pro	Ser	Thr	Pro	Ser	Ser	Ile	Trp	Pro	Gln	Trp	Val	Ile	Leu	Ile	Thr
	115						120					125			
Glu	Leu	Thr	Ile	Pro	Ser	Pro	Ala	His	Gly	Pro	Pro	Trp	Leu	Pro	Asn
	130					135					140				
Ala	Leu	Glu	Arg	Gly	His	Leu	Val	Arg	Glu						
145					150										

<210> 384  
 <211> 557  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
 ggatcctcta gagcggccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60  
 aaagatgtgt tttgttttgg actctctgtg gtcccttcca atgctgtggg tttccaacca 120  
 ggggaagggt cccttttgca ttgccaagt ccataacat gagcactact ctacatggt 180  
 tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240  
 acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300  
 ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360  
 tccccaagac acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420  
 ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaagt 480  
 tcaattgtga aaatgaatat catgcaaata aattatgcga ttttttttcc aaagtaaaaa 540  
 aaaaaaaaaa aaaaaaaa 557

<210> 385  
 <211> 337  
 <212> DNA  
 <213> Homo sapiens

<400> 385  
 ttcccagggt atgtgcgagg gaagacacat ttactatcct tgatggggct gattccttta 60  
 gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120  
 tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180  
 aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240  
 tatcagacag gtccagtttc cgcaccaaca cctgctggtt ccctgtcgtg gtctggatct 300  
 ctttgccac caattcccc ttttccacat cccggca 337

<210> 386  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 386  
 gggcccgcta ccggcccagg ccccgccctcg cgagtccctc tccccgggtg cctgcccgca 60  
 gcccgctcgg ccagaggggt gggcgcgggg ctgcctctac cggctggcgg ctgtaactca 120  
 gcgaccttgg ccggaaggct ctagcaagga cccaccgacc ccagccgcgg cgggcgggc 180  
 gcggactttg ccggtgtgt ggggcggagc ggactgcgtg tccgcggacg ggcagcgaag 240  
 atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

<210> 387  
 <211> 537  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 387

```
gggccgagtc gggcaccaag ggactctttg caggcttcct tcctcggatc atcaaggctg 60
ccccctctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120
tgaaccagga ccggcttctg ggcggctgaa aggggcaagg aggcaaggac cccgtctctc 180
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttcctc agcactgagg 240
gagggggctt gtttcccttc cctcccggcg acaagctcca gggcagggct gtccctctgg 300
gcggcccagc acttcctcag acacaacttc ttctgctgc tccagtcgtg gggatcatca 360
cttaccacc cccaagtgc aagaccaa atctccagctg ccccttcgt gtttccctgt 420
gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctccagcctg ttagtctctc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaaa aaaaaaa 537
```

&lt;210&gt; 388

&lt;211&gt; 520

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 388

```
aggataat ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgagggtaaa ccagtttgca ttccccta atgtgaaaaa taagaggact actcagcact 120
gtttgaagat tgctcttct acagcttctg agaattgtgt tatttcactt gccaaagtga 180
ggacccccct cccaacatgc ccagcccac ccctaagcat ggtcccctgt caccaggcaa 240
ccaggaaact gctacttggt gacctacca gagaccagga gggtttggt agctcacagg 300
acttccccca cccagaaga ttagcatccc atactagact cataactcaac tcaactaggc 360
tcatactcaa ttgatgggta ttagacaatt ccatttcttt ctgggtatta taaacagaaa 420
atctttcttc ttctcattac cagtaaaggc tcttggtatc tttctgttgg aatgatttct 480
atgaacttgt cttattttta tgggtgggtt ttttctggt 520
```

&lt;210&gt; 389

&lt;211&gt; 365

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 389

```
cgttgcccc gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagtttaaggc tggatttcag atctgcctgg ttccagccgc agtgtgccct ctgctcccc 120
aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ctttctctg cttcagcaa gggcggtgc ccacattctc 300
tgagggtcag tggaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365
```

&lt;210&gt; 390

&lt;211&gt; 221

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(221)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 390

```
tgctctcca tcctggcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacggnnt ctcattgggtg tggaacatct ctgcttgagg tttcaggaag gcctctggct 120
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggtgagg aggagtttaag gctggatttc a 221
```

&lt;210&gt; 391

&lt;211&gt; 325

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(325)  
<223> n = A,T,C or G

<400> 391  
tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60  
ctctcgcgcc cagcctggag ctgctcctgg catctaccaa caatcagncg aggcgagcag 120  
tagccagggc actgctgccca acagccagtc cnnataccat catgtnaccc ggtgngctct 180  
naanttngat ntccanagcc ctacccatcn tagttctgct ctcccaccgg ntaccagccc 240  
cactgcccag gaatcctaca gccagtaccc tgtcccgcag tctctaccta ccagtacgat 300  
gagacctccg gctactacta tgacc 325

<210> 392  
<211> 277  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(277)  
<223> n = A,T,C or G

<400> 392  
atattgttta actccttcct ttatatcttt taacattttc atggngaaaag gttcacatct 60  
agtctcactt nggcnagn gn ctctacttg agtctcttcc ccggcctggn ccagtngnaa 120  
antaccanga accgncatgn cttaanaacn ncctggtttn tgggttnntc aatgactgca 180  
tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240  
ctgaggatac agcgccgcgt cctgtgttgc tggggaa 277

<210> 393  
<211> 566  
<212> DNA  
<213> Homo sapiens

<400> 393  
actagtccag tgtggtggaa ttgcggccg cgctgcacgga caggtcagct gtctggctca 60  
gtgatctaca ttctgaagtt gtctgaaaat gtcttcata ttaaattcag cctaaacgtt 120  
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180  
gagaaggctc agtttgtcca tcagcattat catgatata ggactggta cttgggttaag 240  
gaggggtcta ggagatctgt cccttttaga gacaccttac ttataatgaa gtatttgga 300  
gggtgggttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360  
catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420  
ttctgcctca atgtttactg tgcctttgtt tttgctagtt tgtgttgttg aaaaaaaaaa 480  
cattctctgc ctgagtttta atttttgtcc aaagtattt taatctatac aattaaaagc 540  
ttttgcctat caaaaaaaaa aaaaaa 566

<210> 394  
<211> 384  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(384)  
<223> n = A,T,C or G

<400> 394  
gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60  
tgcaaatng gaccgggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120  
gcaggaggac cgggctttaa ggagtthta gctgagtgtc actgtagacc ccaaatacca 180  
tcccaagatt atcgggagaa agggggcagt aattacccaa atccggttgg agcatgacgt 240

gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaa ttaccatcac 300  
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360  
tgagcagatg gtttctgagg acgt 384

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgc 60  
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120  
tatcagaggt ttcattcatt cggaattgt ggagtctaag gaaatcatgg cctctgaagt 180  
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240  
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300  
caagttctct ttggaaagcc tgggcatctc ctcactacag acctctgacc atgggacgg 360  
gcagcctggt gagaccatcc aatcccaa ataaatgcac 399

<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

tggagttntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60  
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120  
agacaaggac aacctgttcc ttcataaactc tctagagaaa aaaaggagtt gttagtagat 180  
actaaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240  
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300  
gtttagggga gggagtgagg gataaaaaga ggaaaaaaag aagagtgaga aaacctattt 360  
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt 403

<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397

actagtnacg tgtggtggaa ttcgcgccg cgctcgacct naanccatct ctatagcaaa 60  
tccatccccg ctctgggtg gtnacagaat gactgacaaa 100

<210> 398

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 398

129

```

gcgggccgct cgacagcagt tccgccagcg ctgcccctg ggtggggatg tgetgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

```

&lt;210&gt; 399

&lt;211&gt; 298

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(298)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 399

```

acggaggtgg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
ggggtgccng catggagcgc atgggcgcg gctggggcca cggcatggat cgcgtgggct 120
ccgagatcga gcgcatgggc ctggtcatgg accgcatggg ctccgtggag cgcattgggct 180
ccggcattga gcgcatgggc ccgctgggcc tcgaccacat ggccctccanc attgancgca 240
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcatggg 298

```

&lt;210&gt; 400

&lt;211&gt; 548

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 400

```

acatcaacta cttcctcatt ttaaggatg gcagttccct tcatcccctt ttcctgcctt 60
gtacatgtac atgtatgaaa ttctcttctc ttaccgaact ctctccacac atcacaagggt 120
caaagaacca cagccttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt ttttccacgt ttaaggggcc atggcaggac ttagagttgc gagttaagac 240
tgcagagggc tagagaatta ttcatatag gctttgagge caccatgtc acttatcccg 300
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
gttgccccca taattctggg cctttgttgt ttgttttaat tacttgggca tcccaggaag 420
ctttccagtg atctcctacc atgggcccc ctccctggat caagcccctc ccaggccctg 480
tccccagccc ctctgcccc agcccacccg cttgccttgg tgctcagccc tcccattggg 540
agcaggtt 548

```

&lt;210&gt; 401

&lt;211&gt; 355

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(355)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 401

```

actgtttcca tggtatgttt ctacacattg ctacctcagt gctcctggaa acttagcttt 60
tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120
taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
tataaatgaa tgtgctgaag caaagtgcc atggtggcgg cgaagaagan aaagatgtgt 240
tttgttttgg actctctgtg gtcccttcca atgctgnggg tttccaacca ggggaagggt 300
cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggn tctgc 355

```

&lt;210&gt; 402

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



<220>  
 <221> misc\_feature  
 <222> (1)...(407)  
 <223> n = A,T,C or G

<400> 402  
 atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60  
 tctcacatgc ggtggcatac ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120  
 aaatggaaaa cagaaaaaag caggtgttgc actcctactt tctgacaaaa cagactatgc 180  
 gaataaagat aaaaaagaga aggacattac aaagggtggtc ctgacctttg ataaatctca 240  
 ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa ttgctgagg 300  
 ttgtggagct tctccctgc agagagtccc tgatctcca aaatttggtt gagatgtaag 360  
 gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407

<210> 403  
 <211> 303  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(303)  
 <223> n = A,T,C or G

<400> 403  
 cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaattcc aggcacccaaa 60  
 tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120  
 tagagaacaa gacctactca gtcataaaca aaaaggcaga caccaacatg gatctcatgg 180  
 gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240  
 tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300  
 gga 303

<210> 404  
 <211> 225  
 <212> DNA  
 <213> Homo sapiens

<400> 404  
 aagtgttaact tttaaaaatt tagtggattt tgaaaattct tagaggaaaag taaaggaaaa 60  
 attgttaatg cactcattta cctttacatg gtgaaagtcc tctcttgatc ctacaaacag 120  
 acattttcca ctcggtgttc catagtgtt aagtgtatca gatgtgttg gcatgtgaat 180  
 ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405  
 <211> 334  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(334)  
 <223> n = A,T,C or G

<400> 405  
 gagctgttat actgtgagtt ctactaggaa atcatcaaat ctgagggttg tctggaggac 60  
 ttcaatacac ctccccccat agtgaatcag cttccagggg gtccagtcct tctccttact 120  
 tcatcccccatt cccatgccaa aggaagacc tccctccttg gctcacagcc ttctctagge 180  
 ttccacagtgc ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtgt 240  
 ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgtc cagccccatgt 300  
 cactctccac tctctcannn tggatccccac ccct 334

<210> 406  
<211> 216  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(216)  
<223> n = A,T,C or G

<400> 406  
tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60  
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120  
acnaaacaca aatttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180  
actgccaaag aatnttcaag aaggaggact gccant 216

<210> 407  
<211> 413  
<212> DNA  
<213> Homo sapiens

<400> 407  
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60  
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120  
gtacaacatt gcacccagtgc tcagattcta cacctggcca ctcaggaagc aagagttaat 180  
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240  
ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300  
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360  
tgggagttcc agaaaaagt tttaaacagaca atgggccagg ttctgtagta aag 413

<210> 408  
<211> 183  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(183)  
<223> n = A,T,C or G

<400> 408  
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60  
tnccttaacta gttaatcctt aaagggctan ntaatcctta actagtcctt ccattgtgag 120  
cattatcctt ccagtattcn ccttctnttt tatttactcc ttcttggtta cccatgtact 180  
ntt 183

<210> 409  
<211> 250  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(250)  
<223> n = A,T,C or G

<400> 409  
cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60  
gtggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120  
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180  
gcttcccagt gccccagga cagcgtgggc tatgtttaca ggcntcctt gctggggggg 240  
ggcctatgc 250

<210> 410  
 <211> 306  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(306)  
 <223> n = A,T,C or G

<400> 410  
 ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60  
 agtcttgcaa tcccatttgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120  
 cccagggacc ttggaaacag ttggcactgt aagggtgctt ctccccaaga cacatcctaa 180  
 aagggtgttg aatggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240  
 nactggttgg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300  
 tcntgc 306

<210> 411  
 <211> 261  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(261)  
 <223> n = A,T,C or G

<400> 411  
 agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60  
 ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120  
 tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180  
 aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240  
 cttctctcaa ggngaggcaa a 261

<210> 412  
 <211> 241  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(241)  
 <223> n = A,T,C or G

<400> 412  
 gttcaatggt acctgacatt tctacaacac ccactcacc gatgtattcg ttgccagtg 60  
 ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgccagg aaatactacg 120  
 actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180  
 ctgggagatt tcaactgggtta cattgaattc ccaaactacc cangcaatta cccagccaac 240  
 a 241

<210> 413  
 <211> 231  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(231)  
 <223> n = A,T,C or G

<400> 413  
aactctttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60  
ctcatccaag tttctagtag cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120  
aagtttactc tcctcatttg gaacctaaaa actctcttct tcctgggtct gagggctcca 180  
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414  
<211> 234  
<212> DNA  
<213> Homo sapiens

<400> 414  
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60  
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120  
gtgagccaag gagggagggt cttccttttg catgggatgg ggatgaagta aggagaggga 180  
ctggaccccc tggaagctga ttcactatgg ggggagggtg attgaagtcc tcca 234

<210> 415  
<211> 217  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(217)  
<223> n = A,T,C or G

<400> 415  
gcataggatt aagactgagt atcttttcta cattctttta actttctaag gggcacttct 60  
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttctca 120  
cacctagcaa tagtagaatt cagtctact tctgaggcca gaagaatggt tcagaaaaat 180  
antggattat aaaaaataac aattaagaaa aataatc 217

<210> 416  
<211> 213  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(213)  
<223> n = A,T,C or G

<400> 416  
atgcatatnt aaagganact gcctcgcttt tagaagacat ctggngctgct ctctgcatga 60  
ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120  
cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180  
atattggaac agatggagtc tctactacaa aag 213

<210> 417  
<211> 303  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(303)  
<223> n = A,T,C or G

<400> 417  
nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60

```

gtgggaaagg ctttactctg agttcaaata ttcaagccca tcagagagtc cactctggag 120
agaagccata caaatgcaat gagggtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240
tcantcaaag ttcgtatctt caaatccatc ngaagggncca cagtatanan aaacctttta 300
agt 303

```

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<210> 418
<211> 328
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

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```

<400> 418
tttttggcgg tgggtggggca gggacggggac angagtctca ctctgttgcc caggctggag 60
tgcacaggca tgatctcggc tcaactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180
gtatttttag tagagacagg gtttcacccat gttggccagg ctggtctcaa actcctnacc 240
tcagnggtca ggctgggtct aaactcctga cctcaagtga tctgcccacc tcagcctccc 300
aaagtgtan gattacaggc cgtgagcc 328

```

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<210> 419
<211> 389
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

```

```

<400> 419
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatatg 60
acccctgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttggttctt ctctgtggct ccattcatag cacagttgtt gcaactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240
ccggttctcc agccaccaac ctcaactcgt cccgcaaagt gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360
tggcagccac tcnggctgtg tcgacgcgg 389

```

```

<210> 420
<211> 408
<212> DNA
<213> Homo sapiens

```

```

<400> 420
gttcctccta actcctgcc aaaaacagct tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtt tcttggttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtgtg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgaccca taaagggaat ctcattggca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat ggtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgtatg aaaaacctgg caagcccg 408

```

```

<210> 421
<211> 352
<212> DNA
<213> Homo sapiens

```

<220>  
 <221> misc\_feature  
 <222> (1)...(352)  
 <223> n = A,T,C or G

<400> 421  
 gctcaaaaat ctttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60  
 gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120  
 ttacttgaca gaacaggtct tttttgggtc cttcttctcc accacnatac atttgagtc 180  
 ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacaggtg tagaaacaag 240  
 ggtgcaacat gaaatttctg tttcgtagca agtgcattgc tcacaagttg gcangtctgc 300  
 cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg 352

<210> 422  
 <211> 337  
 <212> DNA  
 <213> Homo sapiens

<400> 422  
 atgccaccat gctggcaatg cagcggggcg tcgaaggcct gcatatccag cccaagctgg 60  
 cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120  
 gcgatagcaa ggtgccggcg atcgcggcg cgccaatcct ggccaaggtc agccgtgac 180  
 gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggct 240  
 atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300  
 gcttcttccg ccggtacggc tggcctatga aaattat 337

<210> 423  
 <211> 310  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(310)  
 <223> n = A,T,C or G

<400> 423  
 gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60  
 aggagaatga ggcctggcct gggagccctg tgccactan aagcncatta gattatccat 120  
 tcaactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtc 180  
 tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240  
 gtgcaacatg aaatttctgt ttcgtagcaa gtgcattgtc cacagttgtc aagtctgcc 300  
 tccgagttta 310

<210> 424  
 <211> 370  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(370)  
 <223> n = A,T,C or G

<400> 424  
 gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60  
 ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120  
 cactgacaga acaggtcttt tttgggtcct tcttctccac cagcatatac ttgcagtcct 180  
 ccttcttgaa gattcttttg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240  
 ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300  
 cacgaagggtg gcaaagatca caacgtgcc cagganaaca ttcattgtga taagcaggac 360  
 tccgtcgacg 370

<210> 425  
 <211> 216  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(216)  
 <223> n = A,T,C or G

<400> 425  
 aattgctatn ntttattttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaatga 60  
 taacaacnca acatcaaggn aaananaaca ggaatggntg actntgcata aatnggccga 120  
 anattatcca ttatnttaag ggttgacttc aggntacagc acacagacaa acatgcccgag 180  
 gaggnntntca ggaccgctcg atgtntnttg aggagg 216

<210> 426  
 <211> 596  
 <212> DNA  
 <213> Homo sapiens

<400> 426  
 cttccagtga ggataaccct gttgccccgg gccgagggttc tccattaggc tctgattgat 60  
 tggcagtcag tgatggaagg gtgttctgat cattccgact gcccgaaggg tcgctggcca 120  
 gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatgggtga 180  
 gctgtccttg tatttttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240  
 gacatcacgg caacttttaa tgaaatgatt tgaagggccca ttaagaggca cttcccgtta 300  
 ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360  
 aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420  
 ggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agccaggaga 480  
 atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggtc tactgcctga 540  
 gtcccgtggt tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

<210> 427  
 <211> 107  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(107)  
 <223> n = A,T,C or G

<400> 427  
 gaagaattca agtttaggtt attcaaaggg cttacngaga atcctanacc caggncccag 60  
 cccgggagca gccttanaga gctcctgttt gactgcccgg ctcagng 107

<210> 428  
 <211> 38  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(38)  
 <223> n = A,T,C or G

<400> 428  
 gaacttcna anaangactt tattcactat ttacatt

38

<210> 429

<211> 544  
<212> DNA  
<213> Homo sapiens

<400> 429  
ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60  
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120  
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180  
tttgatggt ggctcatcac ctgtagaacc tgacttggtc gtggctggaa tccactcggt 240  
gccttccact tcagttacac ctcaactcacc atcctctcct gttgggttctg tgctgcttca 300  
agatactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360  
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420  
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480  
acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccagggtg gtaggagaga 540  
ttat 544

<210> 430  
<211> 507  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(507)  
<223> n = A,T,C or G

<400> 430  
cttatcncaa tggggctccc aaacttggct gtgcagtga aactccgggg gaattttgaa 60  
gaacactgac acccatcttc caccgcgaca ctctgattta attgggctgc agtgagaaca 120  
gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttgtg atctttgccc 180  
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240  
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300  
caagaaggag gactgcaagt atatcggtgt ggagaagaag gacccaaaaa agacctgttc 360  
tgtcagtga tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420  
cattctctc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480  
ttttgagcaa aaaaaaaaaa aaaaaaa 507

<210> 431  
<211> 392  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(392)  
<223> n = A,T,C or G

<400> 431  
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60  
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120  
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180  
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcctgggtt ttccaacaga 240  
catcattcca gcattctgag attaggnga ttggggatca ttctggagt ggaatgttca 300  
acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360  
gcaatgagtc tggcttttac tctgctgttt ct 392

<210> 432  
<211> 387  
<212> DNA  
<213> Homo sapiens

<220>



<221> misc\_feature  
<222> (1)...(387)  
<223> n = A,T,C or G

<400> 432  
ggatatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60  
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120  
ngtagtccaa gctctcggn a gtccagccac tngaaacat gctcccttta gattaacctc 180  
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240  
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300  
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgta aggaccggga 360  
acaacgtata gaacactgga gtccttt 387

<210> 433  
<211> 281  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(281)  
<223> n = A,T,C or G

<400> 433  
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60  
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120  
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180  
atcgccgtgg ctattcctcn ttgntattac accagnagg ntctctgtnt gccactgggt 240  
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

<210> 434  
<211> 484  
<212> DNA  
<213> Homo sapiens

<400> 434  
ttttaaaata agcatttagt gctcagtcct tactgagtag tctttctctc ccctcctctg 60  
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120  
tgttgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtaga tccatcttgc 180  
tttttcccca ttggaactag tcattaacct atctctgaac tggtagaaaa acatctgaag 240  
agctagtcta tcagcatctg acaggtgaat tggatggttc tcagaacctt ttcacccaga 300  
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaacct 360  
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420  
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480  
ttta 484

<210> 435  
<211> 424  
<212> DNA  
<213> Homo sapiens

<400> 435  
gcgcccgtca gagcaggtca ctttctgcct tccacgtcct ccttcaagga agccccatgt 60  
gggtagcttt caatatcgca gggtcttact cctctgcctc tataagctca aaccaccaa 120  
cgatcgggca agtaaacccc ctccctcgcc gacttcggaa ctggcgagag ttcagcgag 180  
atgggcctgt ggggaggggg caagatagat gagggggagc ggcatgggtc ggggtgacct 240  
cttgagagaga ggaaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggccct 300  
ggtagagacc tttgggggtc tggaaacctc ggactccca tgctctaact cccacactc 360  
gctatcagaa acttaaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420  
aaac 424

<210> 436

<211> 667  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (1)...(667)  
<223> n = A,T,C or G

<400> 436  
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60  
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120  
agcctcttct ggaattcctc tgattttcaa gtctcactct caagttcttg aaaacgaggg 180  
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240  
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300  
gccaggtttg tcatagcact catcaaagtc cggccaacgt ctgtgcttcg aatataaacc 360  
tgttcatgtt tataggactc attcaagaat tttctatata tctttcttat atactctcca 420  
agttcataat gctgctccat gccagctgg tgagttggc caaatccttg tggccatgag 480  
gattccttta tggggtcagt gggaaagggt tcaatgggac ttcgggtctcc atgccgaaac 540  
accaaagtca caaacttcaa ctcttggct agtacacttc ggtctagcca gaaaaaagc 600  
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660  
tgttgag 667

<210> 437  
<211> 693  
<212> DNA  
<213> Homo sapiens

<400> 437  
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acacagccag gtaaggaaag ctggattggc aactaggac tctaccatac cgggttttgt 120  
taaagctcag gttaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180  
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240  
aggtaactcct ctattttcac cctcttgct tctactctct gccagtcaga cctgtgggag 300  
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360  
catttctcca ggttacccta ggtgtcacta ttggggggac agccagcatc ttagctttc 420  
atgtgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480  
acacctaaat gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540  
tcctatttct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600  
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660  
ctgcatcatg tgctctcttg gctgaaaatg acc 693

<210> 438  
<211> 360  
<212> DNA  
<213> Homo sapiens

<400> 438  
ctgcttatca caatgaatgt tctcctgggc agcgttggtga tctttgccac ctctgtgact 60  
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120  
atgtttctac acctgtgggt tatgacaaag acaactgcc aagaatcttc aagaaggagg 180  
actgcaagta tatctgttg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240  
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctctctg 300  
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360

<210> 439  
<211> 431  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

140

&lt;222&gt; (1)...(431)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 439

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gttcctnnta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attccttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcgccgcg 420
aathtagtag t 431

```

&lt;210&gt; 440

&lt;211&gt; 523

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 440

```

agagataaag cttagggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcctttt tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaagtgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcctggaaca tttatgttcc ttttaagaa 420
acaaaaatca aactttacag aaagatttga tgatgtaac acatatagca gctcttgaag 480
tatatatatc atagcaata agtcatctga tgagaacaag cta 523

```

&lt;210&gt; 441

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 441

```

gttcctccta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attccttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcgccgcg 420
aathtagtag 430

```

&lt;210&gt; 442

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 442

```

ctaaggaatt agtagtggtc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcctggaa tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gataacttga aattaatctt ttattgcact tgttttgacc attagctat 180
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc 362

```

&lt;210&gt; 443

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

141

<220>  
<221> misc\_feature  
<222> (1)...(624)  
<223> n = A,T,C or G

<400> 443  
tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60  
ttgaaagaat taaattcaga ggaggggaga gaaagagtag tcagtaggga ctgagcacta 120  
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180  
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240  
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaaacttg cttcctggtt 300  
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaatgaac 360  
taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtac 420  
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480  
agtagagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctggaaaaga 540  
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600  
ttgtccctat ctgctaaaaca gatc 624

<210> 444  
<211> 425  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(425)  
<223> n = A,T,C or G

<400> 444  
gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60  
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120  
ttcattgcta tagcataaca caaaatttgc ataagtgggtg gtcagcaaat ccttgaatgc 180  
tgcttaaatgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240  
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300  
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcacacctg gaagagccaa 360  
ggaggcacca gggcataagt gagtagactt atggtcgacg cggccgcgaa tttagtagta 420  
gtaga 425

<210> 445  
<211> 414  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(414)  
<223> n = A,T,C or G

<400> 445  
catgtttatg ntttttgatt actttgggca cctagtgttt ctaaatcgtc tatcattctt 60  
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120  
tgaaattctt tgcatgtggc agattattgg atgtagtctt ctttaactag catataaatc 180  
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240  
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300  
ggatttttat aatcctactc acaaatgact aggtctctcc tcttgtattt tgaagcagtg 360  
tggtgtgtgg attgataaaa aaaaaaaaaa tgcacgcggc cgcaatttta gtag 414

<210> 446  
<211> 631  
<212> DNA  
<213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(631)  
 <223> n = A,T,C or G

<400> 446  
 acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60  
 tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcagggtgtg 120  
 atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttgttc 180  
 ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240  
 ctgtcatctg tgtggtgggc ctctgcatca caagggccaa actttaggta atagcattgg 300  
 actgagattt gtaaaccttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360  
 gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420  
 taatctaaag ggagcatggt tcacagtggc tggactaccg agagcttggg ctacacaata 480  
 cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccctg catttgtggt 540  
 aatctacacc aatgaaaaca tgtactacag ctatatattga ttatgtatgg atatatattga 600  
 aatagtatac attgtcttga tgttttttct g 631

<210> 447  
 <211> 585  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(585)  
 <223> n = A,T,C or G

<400> 447  
 ccttgggaaa antntcacaa tataaagggt cgtagacttt actccaaatt ccaaaaagggt 60  
 cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120  
 gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180  
 agttcctgaa aggcaggtat agcaactgat cttcagaaaag aggaactgtg tgcaccggga 240  
 tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300  
 ccaggtttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360  
 gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420  
 gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480  
 attcctttat ggggtcagtg ggaaagggtg caatgggact tccgtctcca tgccgaaaca 540  
 ccaaagtcac aaacttcaac tccttggtca gtacacttcg gtcta 585

<210> 448  
 <211> 93  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(93)  
 <223> n = A,T,C or G

<400> 448  
 tgctcgtggg tcattctgan nnccgaactg accntgccag ccctgccgan ggccnccat 60  
 ggctccctag tgccctggag agganggggc tag 93

<210> 449  
 <211> 706  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature

&lt;222&gt; (1)...(706)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 449

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ccaagttcat gctntgtgct ggacgctgga caggggggcaa aagcnnttgc tcgtgggtca 60
ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120
cctggagagg aggtgtctag tcagagagta gtccctggaag gtggcctctg ngaggagcca 180
cggggacagc atcctgcaga tggtcgggcg cgtcccatc gccattcagg ctgcgcaact 240
gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
gtgctgcaag gcgattaagt tgggtaacgc cagggttttc ccagtcncga cgttgtaaaa 360
cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcatgcacg 420
cgtacgtaag cttggatcct ctagagcggc cgcctactac tactaaattc gcggccgcgt 480
cgacgtggga tccnactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
aacaggttga acctgggagg tggagggttg aatgagctga gatcaggccn ctgcncccca 660
gcatggatga cagagtga aa ctccatctta aaaaaaaaaa aaaaaa 706

```

&lt;210&gt; 450

&lt;211&gt; 493

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 450

```

gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
acagttttta aaggtaaaac aacataaaaa gaaatatcct atagtggaaa taagagagtc 120
aaatgaggct gagaacttta caaagggatc ttacagacat gtcgccaata tcaactgcatg 180
agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240
caagtcaagt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
agagacactg tcagagagtt aaaaagttag ttctatccat gaggtgattc cacagtcttc 360
tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggt cgacgcgggc 480
gcgaatttag tag 493

```

&lt;210&gt; 451

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 451

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gggcgcgtcc cattcgccat tcaggctgcg caactgttgg gaagggcgat cgggtcggggc 60
ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300
tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacaa 360
cgcncacagc actcacagct actcaggagg ctgagaacag gttgaacctg ggagggtggag 420
gttgcaatga gctgagatca ggcnctgcn cccagcatg gatgacagag tgaaactcca 480
tcttaaaaaa aaaaaaaaaa a 501

```

&lt;210&gt; 452

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(51)

<223> n = A,T,C or G

<400> 452

agacggtttc accnttataa cnccttttag gatgggnntt ggggagcaag c 51

<210> 453

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(317)

<223> n = A,T,C or G

<400> 453

tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60  
 acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaacccat 120  
 ttcacccana cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca 180  
 taacaaaccc tgctccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240  
 cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300  
 taccatgtc tttatta 317

<210> 454

<211> 231

<212> DNA

<213> Homo sapiens

<400> 454

ttcgaggtag aatcaactct cagagtgtag tttccttcta tagatgagtc agcattaata 60  
 taagccacgc cagctcttg aaggagtctt gaattctcct ctgctcactc agtagaacca 120  
 agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180  
 ccttcctttt tcagtgttcc aaagctcctc acaatttcat gaacaacagc t 231

<210> 455

<211> 231

<212> DNA

<213> Homo sapiens

<400> 455

taccaaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60  
 cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120  
 gtttcaacgc attgatgact tctccaagga tcttcttttg gcacgacca cattcagggg 180  
 caaagaattt ctcatagcac agctcacaat acagggtcctc tttctcctct a 231

<210> 456

<211> 231

<212> DNA

<213> Homo sapiens

<400> 456

ttggcaggta cccttataaa gaagacacca taccttatgc gttattaggt ggaataatca 60  
 ttccattcag tattatcggt attattcttg gagaaacct gtctgtttac tgtaaccttt 120  
 tgcaactcaa ttcctttatc aggaataact acatagccac tatttataaa gccattggaa 180  
 cctttttatt tgggtgcagct gctagtcagt ccctgactga cattgccaaag t 231

<210> 457

<211> 231

<212> DNA

<213> Homo sapiens

<220>

145

<221> misc\_feature  
<222> (1)...(231)  
<223> n = A,T,C or G

<400> 457  
cgagggtaccc aggggtctga aaatctctnn ttantagtc gatagcaaaa ttgttcatca 60  
gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catacagttt 120  
tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180  
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231

<210> 458  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 458  
agggtctggtt cccccactt ccactcccct ctactctctc taggactggg ctgggcccaag 60  
agaagagggg tgggttaggga agccgttgag acctgaagcc ccaccctcta ccttccttca 120  
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180  
ggtcctgggt taggcatttt ggggggccag accccaggag aagaagattc t 231

<210> 459  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 459  
ggtaccgagg ctgctgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60  
ccttcgcgaa acctgtggtg gccaccagt cctaacggga caggacagag agacagagca 120  
gccctgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180  
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 460  
gcagggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60  
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaaat 120  
cccacctccc cacacgcaca cggccagcct ggagcccaca gaaggggcct cctgcagcca 180  
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231

<210> 461  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 461  
cgaggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggaggggtc 60  
gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcctg tgtgtcctgg 120  
gtggggttca gtgaggagtg ggaaattggt tcagcagAAC caagccgttg ggtgaataag 180  
agggggattc catggcactg atagagccct atagtttcag agctgggaat t 231

<210> 462  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 462  
aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60  
gggtcatgca agtataaaaa ttaaaaaaaa aagacttcat gcccaatctc atatgatgtg 120



146

gaagaactgt tagagagacc aacagggtag tgggtagag atttccagag tcttacattt 180  
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231

&lt;210&gt; 463

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 463

tactccagcc tgggtgacaga gcgagaccct atcaccgccc cccacccccc caaaaaaaaa 60  
actgagtaga cagggtgtcct cttggcatgg taagtcttaa gtcccctccc agatctgtga 120  
catttgacag gtgtcttttc ctctggacct cgggtgtcccc atctgagtga gaaaaggcag 180  
tggggagggtg gatcttccag tcgaagcggg atagaagccc gtgtgaaaag c 231

&lt;210&gt; 464

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 464

gtactctaag attttatcta agttgccttt tctgggtggg aaagttaa cttagtgtgact 60  
aaggacatca catatgaaga atgtttaagt tggagggtggc aacgtgaatt gcaaacaggg 120  
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180  
ggtgccagcg caccagctag atgctctgta acttctaggc cccattttcc c 231

&lt;210&gt; 465

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 465

catgttgttg tagctgtggt aatgctggct gcattctcaga cagggttaac ttcagctcct 60  
gtggcaaat agcaacaaat tctgacatca tatttatggt ttctgtatct ttgttgatga 120  
aggatggcac aatttttgct tgtgttcata atatactcag attagttcag ctccatcaga 180  
taactggag acatgcagga cattagggta gtgtttagc tctggtaatg a 231

&lt;210&gt; 466

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 466

caggtagctc tttccattgg atactgtgct agcaagcatg ctctccgggg tttttttaat 60  
ggccttcgaa cagaacttgc cacataccca ggtataatag tttctaacat ttgcccagga 120  
cctgtgcaat caaatattgt ggagaattcc ctactgtgag aagtcacaaa gactataggc 180  
aataatggag accagtccca caagatgaca accagtcggt gtgtgcggct g 231

&lt;210&gt; 467

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 467

gtacaccctg gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg 60  
tgggtgcttt tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac 120  
tgtgccttaa cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180  
gcatgggtct ctgcccaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt 240  
tgtgacctgc tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga 300  
ctgcagcaga c 311

&lt;210&gt; 468

&lt;211&gt; 3112

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 468

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cattgtgttg ggagaaaaac agaggggaga tttgtgtggc tgcagccgag ggagaccagg 60
aagatctgca tgggtgggaag gacctgatga tacagagttt gataggagac aattaaaggc 120
tgggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaacg 180
atgggatggc cagagacaca ggagatgagt tggagcaagc tcaataacaa agtggttcaa 240
cgaggacttg gaattgcatg gagctggagc tgaagttag cccaattgtt tactagttag 300
gtgaatgtgg atgattggat gatcatttct catctctgag cctcagggtc cccatccata 360
aaatgggata cacagtatga tctataaagt gggatatagt atgatctact tctactgggtt 420
atltgaagga tgaattgaga taatttattt cagggtgccta gaacaatgcc cagattagta 480
catttgggtg aactgagaaa tggcataaca ccaaatttaa tataatgtcag atgttactat 540
gattatcatt caatctcata gttttgtcat ggcccaattt atcctcactt gtgcctcaac 600
aaattgaact gttaacaaaag gaatctctgg tctctgggtaa tggctgagca ccactgagca 660
tttccattcc agttggcttc ttgggtttgc tagctgcctc actagtcctc ttaaataaat 720
gaagttttta catttctcca gtgatttttt tatctcacct ttgaagatac tatgttatgt 780
gattaaataa agaacttgag aagaacaggt ttcattaaac ataaaatcaa tgtagacgca 840
aattttctgg atgggcaata cttatgttca caggaaatgc tttaaaatat gcagaagata 900
attaaatggc aatggacaaa gtgaaaaact tagacttttt tttttttttt ggaagtatct 960
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&lt;210&gt; 469

&lt;211&gt; 2229

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 469

```

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tatttctttc aattaactac aaggacaaac acatctcaaa gttgagataa gtgaccagta 120
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tttgactgc atgaattctg tgaaaagctt gttggatatt gtgatagaga tagagaaatg 240
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ccttctttgc atgaagtaag atagtcaact tattcaaaac tttacatcat tctagattta 480
agagacaagg aagagcttct caggcagaag gaataatgta tgcctgacat gttcaaggaa 540
ttacaagtta gattttgttt aggtgcatgg gaggggttga tgggtgatgac agataaggct 600
ggagggtagg ggagaggctg tggctgtata cagcctcagt acaaggctaa gcattttaac 660
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aatggaatt

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&lt;210&gt; 470

&lt;211&gt; 2426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 470

```

gtaaattctt tattgccagg agtgaaccct aaagtggctc acaagagtgc cctatttctt 60
tcaattaaact acaaggacaa acacatctca aagttgagat aagtgaccag tatgatttgc 120
caaaattcta aagcgactc accatgaaat ggataaagg tacccttggg gatttgcact 180
gcatgaattc tgtgaaaagc ttgttgata ttgtgataga gatagagaaa tgaagtatat 240
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ccataaacat tccctctgtg gctcttgcatt tcatatatatt tatctaaact cttataatca 360
aattacactt ttagtatttg ctgtctcatg tgatgatgaa tctcatatgt gtcccttctt 420
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aggaagagct tctcaggcag aaggaataat gtatgcctga catgttcaag gaattacaag 540
ttagattttg tttagggtgca tgggaggggt tgatggtgat gacagataag gctggaggga 600
tggggagagg ctgtggctgt atacagcctc agtacaaggc taagcatttt aactttatac 660
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caaaaatatgt aattaaattc ccatagctgc atgtaacatt gaattcttcc aggttaaaaa 780
aaaaagttaa tctgtgata ttaatggaat gacattttga ggtcttgaga atgggcacaa 840
aagtgggaaa tgaatttcag tatgggcaaa gacactgagg atgatgttga ttagataatt 900
cactccgtaa tgatcatgct gtgtgctagt aagtataacc ctggaaagat cttgagatgc 960

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<210> 471
<211> 812
<212> DNA
<213> Homo sapiens

```

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<400> 471
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aatattaaa aatgagtgtg gctggatata tggagaatgt tgggccaga aggaaccgta 120
gagatcagat attacaacag ctttgttttg agggtagaa atatgaaatg atttggttat 180
gaacgcacag tttaggcagc agggccagaa tcctgaccct ctgccccgtg gttatctcct 240
ccccagcttg gctgcctcat gtcacacag tattccattt tgtttgttg atgtcttctg 300
aagccatcaa gattttctcg tctgttttcc tctcattggt aatgctcact ttgtgacttc 360
atttcaaata tgtaatcccg ttcaaataaa tatccacaac aggatctgtt ttctgcccac 420
tcctttaagg aacacatcaa ttcattttct aatgtccttc ctcacaagc gggaccaggc 480
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gtgcttctt ttgtgcttcc tgtgtgtgtg gatattttaa ggggctggaa atgtgcaaaa 600
acatgtcact acctagacat tatattgtca tcttctgtt tctagtgatg ttaattatct 660
ccatttcagc agatgtgtgg cctcagatgg taaagtcagc agcctttctt atttctcacc 720
tctgtatcat caggtccttc ccaccatgca gatcttctct gtctccctcg gctgcagcca 780
cacaatatct ccctctgttt ttctgatgcc ag

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<210> 472
<211> 515
<212> DNA
<213> Homo sapiens

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<220>
<221> misc feature
<222> (1)...(515)
<223> n = A,T,C or G

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<400> 472
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cttatgactt tcctatcatg cttattaata aataatacag cccagagaag atgaaaatgg 120
gttccagaat tattggctct tgagcccgg tgaatctcag caagaggaa caccaactga 180
caatcaggat attgaacctg gacaagagag agaaggaaca cctccgatcg aagaacgtaa 240

```

150

```

agtagaaggt gattgccagg aaatggatct ggaaaagact cggagtgagc gtggagatgg 300
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agatgggcag ccataagtta aaaagaagac aagctgaagc tacacacatg gctgatgtca 420
cattgaaaat gtgactgaaa atttgaaaat tctctcaata aagtttgagt tttctctgaa 480
gaaaaaaaaa naaaaaaaaa aaanaaaan aaaaa                    515

```

&lt;210&gt; 473

&lt;211&gt; 750

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 473

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Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
      5                      10                      15

Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
      20                      25                      30

Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
      35                      40                      45

Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
      50                      55                      60

Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
      65                      70                      75                      80

Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
      85                      90                      95

Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
     100                      105                      110

Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
     115                      120                      125

Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
     130                      135                      140

Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
     145                      150                      155                      160

Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
      165                      170                      175

Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
     180                      185                      190

Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
     195                      200                      205

Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
     210                      215                      220

Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
     225                      230                      235                      240

Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
     245                      250                      255

Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr

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260					265					270					
Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	Ala	Val	Gly
		275					280					285			
Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	Asp	Ala	Gln	Lys
		290				295					300				
Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp	Ser	Ser	Trp	Arg
		305				310					315				320
Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Thr	Gly	Asn
				325					330					335	
Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Thr	Asn	Glu	Val
			340					345					350		
Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro
		355					360					365			
Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly
		370				375					380				
Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg
		385				390					395				400
Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile
				405					410					415	
Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr
			420					425					430		
Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala
		435					440					445			
Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val
		450				455					460				
Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu
		465				470					475			480	
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu	Ser
				485					490					495	
Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	Arg	Ile
			500					505					510		
Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln	Arg	Leu
		515					520					525			
Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Glu	Thr	Asn
		530				535					540				
Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	Tyr	Glu	Thr	Tyr	Glu
				545		550					555				560
Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	Lys	Tyr	His	Leu	Thr	Val
				565					570					575	
Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser	Ile	Val
			580					585					590		

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala  
 595 600 605  
 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr  
 610 615 620  
 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr  
 625 630 635 640  
 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser  
 645 650 655  
 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu  
 660 665 670  
 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg  
 675 680 685  
 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser  
 690 695 700  
 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp  
 705 710 715 720  
 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala  
 725 730 735  
 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala  
 740 745 750

<210> 474  
 <211> 386  
 <212> PRT  
 <213> Homo sapiens

<400> 474  
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 Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala  
 20 25 30  
 Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser  
 35 40 45  
 Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro  
 50 55 60  
 Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu Gln His Tyr Glu  
 65 70 75 80  
 Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser  
 85 90 95  
 Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr  
 100 105 110  
 Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly  
 115 120 125  
 Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His

153

130                      135                      140  
 Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu Pro Phe Arg Asn  
 145                      150                      155                      160  
 Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu Lys Ser Glu Glu  
                     165                      170                      175  
 Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile Ala Thr Leu Gly  
                     180                      185                      190  
 Lys Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly Ile Trp Ser Lys  
                     195                      200                      205  
 Val Tyr Asp Pro Leu Tyr Cys Glu Ser Val His Asn Phe Thr Leu Pro  
                     210                      215                      220  
 Ser Trp Ala Thr Glu Asp Thr Met Thr Lys Leu Arg Glu Leu Ser Glu  
 225                      230                      235                      240  
 Leu Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser  
                     245                      250                      255  
 Arg Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Asn His Met Lys  
                     260                      265                      270  
 Arg Ala Thr Gln Ile Pro Ser Tyr Lys Lys Leu Ile Met Tyr Ser Ala  
                     275                      280                      285  
 His Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn  
                     290                      295                      300  
 Gly Leu Leu Pro Pro Tyr Ala Ser Cys His Leu Thr Glu Leu Tyr Phe  
 305                      310                      315                      320  
 Glu Lys Gly Glu Tyr Phe Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln  
                     325                      330                      335  
 His Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys Ser Pro Ser Cys Pro  
                     340                      345                      350  
 Leu Glu Arg Phe Ala Glu Leu Val Gly Pro Val Ile Pro Gln Asp Trp  
                     355                      360                      365  
 Ser Thr Glu Cys Met Thr Thr Asn Ser His Gln Gly Thr Glu Asp Ser  
                     370                      375                      380  
 Thr Asp  
 385

&lt;210&gt; 475

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 475

Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly  
                     5                      10                      15

Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu  
                     20                      25                      30





Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val Leu Val His Pro  
 50 55 60  
 Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val Ile  
 65 70 75 80  
 Leu Leu Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln Val  
 85 90 95  
 Phe Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp Met Ser Leu  
 100 105 110  
 Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser His Asp Leu  
 115 120 125  
 Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala Val Lys  
 130 135 140  
 Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys Tyr  
 145 150 155 160  
 Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Phe Leu Thr Pro Lys  
 165 170 175  
 Lys Leu Gln Cys Val Asp Leu His Val Ile Ser Asn Asp Val Cys Ala  
 180 185 190  
 Gln Val His Pro Gln Lys Val Thr Lys Phe Met Leu Cys Ala Gly Arg  
 195 200 205  
 Trp Thr Gly Gly Lys Ser Thr Cys Ser Gly Asp Ser Gly Gly Pro Leu  
 210 215 220  
 Val Cys Asn Gly Val Leu Gln Gly Ile Thr Ser Trp Gly Ser Glu Pro  
 225 230 235 240  
 Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr Lys Val Val His Tyr  
 245 250 255  
 Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn Pro Gly Ser Met Ala  
 260 265 270  
 Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile Leu Gly  
 275 280 285  
 Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly  
 290 295 300  
 Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met  
 305 310 315 320  
 Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val  
 325 330 335  
 Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly  
 340 345 350  
 Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu  
 355 360 365  
 Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala  
 370 375 380

Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp  
 385 390 395 400  
 Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn  
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 Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro  
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 Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys  
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 Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly  
 450 455 460  
 Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro  
 465 470 475 480  
 Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala  
 485 490 495  
 Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys  
 500 505 510  
 Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser Glu Phe Met Val  
 515 520 525  
 Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala Gln Leu  
 530 535 540  
 Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu Ala Ala  
 545 550 555 560  
 Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu  
 565 570 575  
 Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val  
 580 585 590  
 Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr  
 595 600 605  
 Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu  
 610 615 620  
 Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys  
 625 630 635 640  
 Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly  
 645 650 655  
 Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu  
 660 665 670  
 Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser  
 675 680 685  
 Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu  
 690 695 700  
 Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr

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Gln Glu Glu Cys	Leu Phe Gly Leu Leu Thr	Leu Ile Phe Leu Thr Cys				
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Val Ala Ala Thr	Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr					
	740		745			750
Glu Pro Ala Glu Gly Leu Ser	Ala Pro Ser Leu Ser Pro His Cys Cys					
	755		760			765
Pro Cys Arg Ala Arg Leu	Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro					
	770		775			780
Arg Leu His Gln Leu Cys Cys Arg Met Pro	Arg Thr Leu Arg Arg Leu					
	785		790			800
Phe Val Ala Glu Leu Cys Ser Trp Met	Ala Leu Met Thr Phe Thr Leu					
	805		810			815
Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg						
	820		825			830
Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg						
	835		840			845
Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe						
	850		855			860
Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val						
	865		870			880
Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys						
	885		890			895
Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly						
	900		905			910
Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu						
	915		920			925
Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr						
	930		935			940
Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly						
	945		950			955
Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly						
	965		970			975
Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys						
	980		985			990
Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val						
	995		1000			1005
Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala						
	1010		1015			1020
Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val						
	1025		1030			1035
						1040

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Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu  
1045 1050 1055

Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser  
1060 1065 1070

Asp Leu Ala Lys Tyr Ser Ala  
1075

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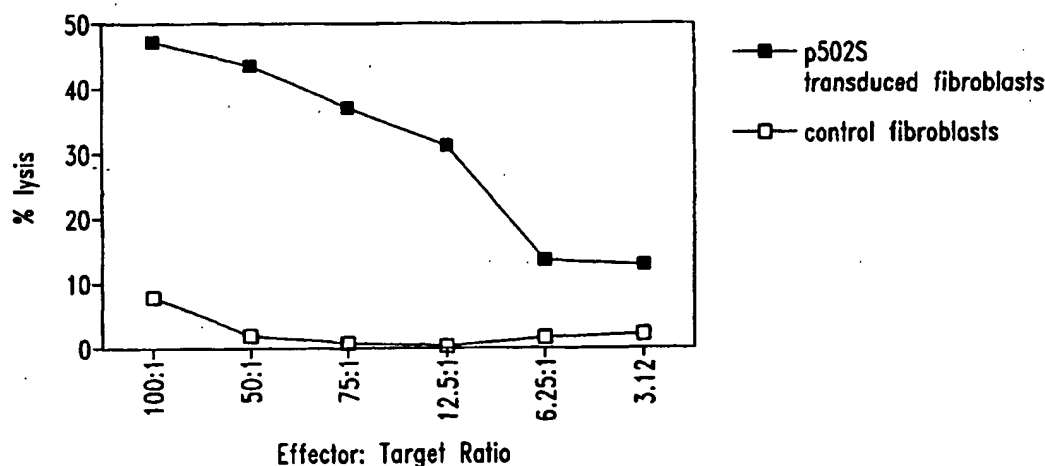
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ning of each regular issue of the PCT Gazette.

(54) Title: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.

WO 01/25272 A3

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/27464

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N15/62 C07K14/47 C07K16/30 C12Q1/68  
G01N33/68 G01N33/547 A61K39/00 A61K39/395 A61P35/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12Q G01N A61K A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WO 98 37093 A (CORIXA CORPORATION) 27 August 1998 (1998-08-27)</p> <p>see especially SEQ ID NOS: 2, 3, 107 and 108 the whole document</p> <p>---</p> <p>-/--</p>	<p>1-15, 17-19, 21,22, 29-31, 34,35, 39-42, 44-46, 48,49, 53-55, 58-79</p>

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

19 January 2001

Date of mailing of the international search report

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Name and mailing address of the ISA

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/27464

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 37418 A (CORIXA CORPORATION) 27 August 1998 (1998-08-27)  see especially SEQ ID NOS: 2, 3, 107 and 108 the whole document ---	1-15, 17-19, 21,22, 29-31, 34,35, 39-42, 44-46, 48,49, 53-55, 58-79
X	EMBL database, Heidelberg, FRG Emhum1 accession number AF047020 20 February 1998 ALBERS, C. ET AL.: "Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds." XP002157763 the whole document -& EMBL database, Heidelberg, FRG Trembl accession number 043673 01 June 1998 ALBERS, C. ET AL.: "ALPHA-METHYLACYL-COA RACEMASE (EC 5.1.99.4)" XP002157764 the whole document ---	1,4,5, 7-12
P,X	WO 00 04149 A (CORIXA CORPORATION) 27 January 2000 (2000-01-27) see especially SEQ ID NOS: 2, 3, 107 and 108 the whole document ---	1-79
A	US 5 925 362 A (SPITLER, L.E. ET AL.) 20 July 1999 (1999-07-20)  the whole document ---	35, 39-49, 53-57
A	SJÖGREN, H.O.: "Therapeutic immunization against cancer antigens using genetically engineered cells" IMMUNOTECHNOLOGY, vol. 3, no. 3, October 1997 (1997-10), pages 161-172, XP004097000 the whole document ---	23-28, 32-34, 53-57
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	-/--	



# INTERNATIONAL SEARCH REPORT

International Application No

PLI/US 00/27464

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>CHU, R.S. ET AL.: "CpG Oligodeoxynucleotides Act as Adjuvants that Switch on T Helper 1 (Th1) Immunity" JOURNAL OF EXPERIMENTAL MEDICINE, vol. 186, no. 10, 17 November 1997 (1997-11-17), pages 1623-1631, XP002910130 the whole document</p> <p>---</p>	<p>14-16, 18-20, 25-27, 41-43, 45-47</p>
A	<p>EP 0 317 141 A (BECTON DICKINSON AND COMPANY) 24 May 1989 (1989-05-24) the whole document</p> <p>-----</p>	<p>50-52</p>

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 00/27464

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  

Although claims 29-34, 48, 49, 52 and 55-57 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-79 PARTIALLY

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

## 1. Claims: 1-79 partially

## Invention 1

An isolated polypeptide comprising at least an immunogenic portion of a prostate tumor protein as defined by the SEQ ID NO: 108 (corresponding to clone F1-12), wherein said polypeptide being encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 2, 3 and 107 (each corresponding to clone F1-12), fragments or variants of said polypeptide, fusion proteins comprising said polypeptide, polynucleotides or oligonucleotides derived from said polynucleotides, antibodies or fragments thereof binding to said polypeptide, pharmaceutical compositions or vaccines comprising said products and their use in methods for inhibiting, monitoring or diagnosing the development of a prostate cancer, for removing tumor cells from a sample or for expanding and / or stimulating T-cells;

## 2. Claims: 1-79 partially

## Invention 2

Idem as subject 1 but limited to the clone J1-17 (SEQ ID NOS: 8, 9, 109 and 112);

## 3.-445. Claims: 1-79 partially (as far as applicable)

## Inventions 3-445

Idem as subject 1 but limited to SEQ ID NOS: 1, 4-7, 10-106, 110, 111, 113-305, 307-315, 326-335, 339-375 and 381-472.

## INTERNATIONAL SEARCH REPORT

information on patent family members

International Application No

PCT/US 00/27464

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